

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 12:30:45 ; Search time 8558.13 Seconds
(without alignments)
11051.408 Million cell updates/sec

Title: US-09-820-095B-3_COPY_1_2000
Perfect score: 2000
Sequence: 1 tctccaagtccatggtgccc.....agctcggtcagctgcca 2000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364494745 residues

Total number of hits satisfying chosen parameters: 9053459

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb.ba.*
2: gb.btg.*
3: gb.in.*
4: gb.om.*
5: gb.cv.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2000	100.0	28984	9	AB002059 Homo sapi
2	2000	100.0	147086	9	AC002472 Homo sapi
3	2000	100.0	162470	9	AC007664 Homo sapi
4	1624.6	81.2	175167	2	AC116044 Papio ham
5	1025.4	51.3	147086	9	AC002472 Homo sapi
6	1025.4	51.3	162470	9	AC007664 Homo sapi
7	563	28.1	563	6	CQ073030 Sequence
8	563	28.1	563	6	CQ103845 Sequence
9	563	28.1	563	6	CQ142655 Sequence
10	563	28.1	563	6	CQ178146 Sequence
11	563	28.1	563	6	CQ225890 Sequence
12	563	28.1	563	6	CQ263940 Sequence
13	563	28.1	563	6	CQ301025 Sequence
14	563	28.1	563	6	CQ338301 Sequence
15	554	27.7	554	6	CQ103739 Sequence
16	554	27.7	554	6	CQ178050 Sequence
17	554	27.7	554	6	CQ300915 Sequence
18	458.4	22.9	1904	6	AX714692 Sequence
19	458.4	22.9	1904	9	AK057257 Homo sapi

C 20	364.4	18.2	1828	9	BC009991
C 21	288	14.4	288	11	G03785
C 22	158.4	7.9	160	6	AX907126
C 23	158.4	7.9	160	6	BD042659
C 24	141	7.0	792	6	CQ732492
C 25	139	7.0	139	6	CQ116544
C 26	139	7.0	139	6	CQ187685
C 27	139	7.0	139	6	CQ313092
C 28	115.4	5.8	201300	9	AL137073
C 29	114	5.7	3226	9	AK128646
C 30	109.2	5.5	123817	9	AL713980
C 31	109.2	5.5	151964	9	AL663038
C 32	109.2	5.5	174327	2	AL672191
C 33	109.2	5.5	198550	9	AC012170
C 34	106.2	5.4	107967	9	AL353701
C 35	107.4	5.4	72402	9	AL389924
C 36	107.2	5.4	160702	9	AC090937
C 37	107.2	5.4	181321	9	AC093179
C 38	106.6	5.3	136270	9	AC005283
C 39	106.6	5.3	163795	9	AP000356
C 40	106.6	5.3	186858	9	AL356585
C 41	106.4	5.3	141628	9	AL391724
C 42	106.4	5.3	172413	2	AC134388
C 43	106.4	5.3	186044	2	AC084099
C 44	106.4	5.3	191500	2	AC145062
C 45	106.4	5.3	198947	2	AC105308

ALIGNMENTS

RESULT 1
AB002059
LOCUS Homo sapiens DNA for Human P2XM, complete cds.
DEFINITION AB002059.1 GI:2350848
VERSION Human P2XM.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Urano,T., Nishimori,H., Han,H., Furuhata,T., Kimura,Y., Nakamura,Y.
TITLE Cloning of P2XM, a novel human P2X receptor gene regulated by p53
JOURNAL Cancer Res. 57 (15), 3281-3287 (1997)
MEDLINE 97384966
PUBMED 9242461
REFERENCE 2 (bases 1 to 28984)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1997) Yusuke Nakamura, The Inst. of Medical
Science, The University of Tokyo, Lab. of Molecular Medicine, Human
Genome Center, 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
E-mail:yusuke@ims.u-tokyo.ac.jp, Tel:81-3-5449-5372,
Fax:81-3-5449-5433
Location/Qualifiers
1. 28984
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="22"
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19708..19801,19914..19979,20155..20232,20323..20520)
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/gene="HP2XM"
/codon_start=1

OK 73019, USA
17 (bases 1 to 147086)
Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
Direct Submission
Submitted (09-APR-2003) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Oct 19, 2002 this sequence version replaced gi:22597497.
Because these overlapping clones came from different libraries.

FEATURES
source
Location/Qualifiers
1..147086
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="22"
/map="22q11.2"
/clone="p_n5"

ORIGIN

Query Match 100.0%; Score 2000; DB 9; Length 147086;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 57315 TCTCCAAATCCATGGTGGCTGGTAGGACAGAGGGGGATGATGTGAACCCCTGCATGC 57374

QY 61 TATAGCCACTGCCTCCCTCCCTGCGCTGCACTACTGCGCCCTATTTTGGCTCTAG 120
DB 57375 TATAGCCACTGCCTCCCTCCCTGCGCTGCACTACTGCGCCCTATTTTGGCTCTAG 57434

QY 121 AAGCACTGCTTCTATGCTTCTAGGACCACTGCGCGCATATGACAGATGAACATCGA 180
DB 57435 AAGCACTGCTTCTATGCTTCTAGGACCACTGCGCGCATATGACAGATGAACATCGA 57494

QY 181 GGCTAAGGCAACGCAATCTTTTCTTAAAGTCATACAGCTGTCTAAAGAAAGCTGGACA 240
DB 57495 GGCTAAGGCAACGCAATCTTTTCTTAAAGTCATACAGCTGTCTAAAGAAAGCTGGACA 57554

QY 241 ACTGGGCAACATAGCGATATAAAATTTATTTAAATTTAGCCAGATGGTAGCCCTG 300
DB 57555 ACTGGGCAACATAGCGATATAAAATTTATTTAAATTTAGCCAGATGGTAGCCCTG 57614

QY 301 TAGTCTCAGGCTCAGGAGGCTAGGAGGAGGCTCACCAGCTCAGAGTTCAGGAT 360
DB 57615 TAGTCTCAGGCTCAGGAGGCTAGGAGGAGGCTCACCAGCTCAGAGTTCAGGAT 57674

QY 361 GCAGTGAGCTATGATCCTGCCACTGCATCTGAAGCTGGGTGACAGAGCAAGACCTGGCT 420
DB 57675 GCAGTGAGCTATGATCCTGCCACTGCATCTGAAGCTGGGTGACAGAGCAAGACCTGGCT 57734

QY 421 CTAATAATGAATACATAAAGTCTCAGAGTCTAGTGGTAGCTTAATCTCCAGAGTCAGG 480
DB 57735 CTAATAATGAATACATAAAGTCTCAGAGTCTAGTGGTAGCTTAATCTCCAGAGTCAGG 57794

QY 481 CTCCTACCTGTCTGATGACAAATGGACACTATGCTTTTAACTGATTGACAGACACAAA 540
DB 57795 CTCCTACCTGTCTGATGACAAATGGACACTATGCTTTTAACTGATTGACAGACACAAA 57854

QY 541 TGTTTTGTGAATATTTTCCAGGAAATAAACCAGAGTCTGATTGCAATTTTACAGGGGG 600
DB 57855 TGTTTTGTGAATATTTTCCAGGAAATAAACCAGAGTCTGATTGCAATTTTACAGGGGG 57914

QY 601 ATTATATTAGTTTACCTGTGGATTGGGAAACCCAGCTCTGATTGCAATTTTACAGGGGG 660
DB 57915 ATTATATTAGTTTACCTGTGGATTGGGAAACCCAGCTCTGATTGCAATTTTACAGGGGG 57974

QY 661 ACAGCCTTTGGTGCACTGTCTGGCGGATTTTCAATTTTAACTCTCTTAGAAGCGCT 720
DB 57975 ACAGCCTTTGGTGCACTGTCTGGCGGATTTTCAATTTTAACTCTCTTAGAAGCGCT 58034

QY 721 TCTCATGTGTAAGTTCCTGATGCGCCAGGAGCGCCGAGGAGGGGCTGGAGA 780
DB 58035 TCTCATGTGTAAGTTCCTGATGCGCCAGGAGCGCCGAGGAGGGGCTGGAGA 58094

QY 781 CGCCCCGACAGAGGCTACGTGCCCTCTGACAGAGAGTCTCTGCTCTCTCGCGCGGCC 840
DB 58095 CGCCCCGACAGAGGCTACGTGCCCTCTGACAGAGAGTCTCTGCTCTCTCGCGCGGCC 58154

QY 841 AGCCCACTCCCAACACCCCTGCGGAGAAAGCCCCCAAGGGAGGAGAGCGGCTGGCCC 900
DB 58155 AGCCCACTCCCAACACCCCTGCGGAGAAAGCCCCCAAGGGAGGAGAGCGGCTGGCCC 58214

QY 901 CTGCCCCGAGACCTTCGGTCTTAGGTGAGTCTGAATCGGCTTGGGACCTGCTCTG 960
DB 58215 CTGCCCCGAGACCTTCGGTCTTAGGTGAGTCTGAATCGGCTTGGGACCTGCTCTG 58274

QY 961 GCTTGGGGACCCCTGCACAGCGTCCACAGGCGCGCTCGCTCTCTCTCTCTCTCTTTTA 1020
DB 58275 GCTTGGGGACCCCTGCACAGCGTCCACAGGCGCGCTCGCTCTCTCTCTCTCTTTTA 58334

QY 1021 TCTTCCCGACCTCTGGCAGGAAACCGCTCATGTTACGCCCCCTTTCGAGCGCTCAGACC 1080
DB 58335 TCTTCCCGACCTCTGGCAGGAAACCGCTCATGTTACGCCCCCTTTCGAGCGCTCAGACC 58394

QY 1081 CTGAGCGGAGACCGCTTGGCGCTCCTACTTAGAGCGGACCCGCGGATGTGGCGGAGTC 1140
DB 58395 CTGAGCGGAGACCGCTTGGCGCTCCTACTTAGAGCGGACCCGCGGATGTGGCGGAGTC 58454

QY 1141 TGGCGTGGCTGACCAATCGAGTGTGGCTCATCGACTGGCGTCTGCCACGGCAATTA 1200
DB 58455 TGGCGTGGCTGACCAATCGAGTGTGGCTCATCGACTGGCGTCTGCCACGGCAATTA 58514

QY 1201 GCGACGGCTCCCGCGGCGGTCGCGCGGCAACCCAGTGTGTAGTTCGCTAGAA 1260
DB 58515 GCGACGGCTCCCGCGGCGGTCGCGCGGCAACCCAGTGTGTAGTTCGCTAGAA 58574

QY 1261 CCGTGGCTCTCTCTGCGCTCAGGCTCTCGCTGAGAGGATAAATGCACGCGCCACGGGC 1320
DB 58575 CCGTGGCTCTCTCTGCGCTCAGGCTCTCGCTGAGAGGATAAATGCACGCGCCACGGGC 58634

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DB 58635 TATGCACTGGCTGGCGCTTGTGGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 58694

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DB 58695 CGCCCCCTTTTCTGCTGACTGGGAAACACGCTTACCTCCAGGACTTGTGTGTCTCTCTCTG 58754

QY 1441 CACTGGGAGTGGCGGGGAGCTTTTTCAGAGGGCTGGGAACTTCGAGAGCCAG 1500
DB 58755 CACTGGGAGTGGCGGGGAGCTTTTTCAGAGGGCTGGGAACTTCGAGAGCCAG 58814

QY 1501 GTCACT 1560
DB 58815 GTCACT 58874

QY 1561 CTCCCTGCACCGAAACCTCCATCCCATCTTTTGTCTGTCTGCTGCAACTTCGAAATCTG 1620
DB 58875 CTCCCTGCACCGAAACCTCCATCCCATCTTTTGTCTGTCTGCTGCAACTTCGAAATCTG 58934

QY 1621 CAAGGTGAGCTTAGAGTCACTCTTCGGAAGCTTCTCAACACCTCCCGCGCTG 1680
DB 58935 CAAGGTGAGCTTAGAGTCACTCTTCGGAAGCTTCTCAACACCTCCCGCGCTG 58994

QY 1681 CTGCT 1740
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QY 1741 CCAACCACTCTCACTCCGACCCGAGAGTGAAGGCGAGGCGGAGGAGAGTCTGCTGC 1800
DB 59055 CCAACCACTCTCACTCCGACCCGAGAGTGAAGGCGAGGCGGAGGAGAGTCTGCTGC 59114

QY 1801 TGTTCCTCTGTGCGACAGGCGCCAGCAAGGGAAATCTAGGAGGGTGGGAGGTGCAGGGCA 1860
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QY 1081 CTGAGCGGAGACCGCTTCGGCCCTCCTCCTAGAGCGGACCGCGGATGTGGCGGATC 1140
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QY 1441 CACTGGGAGAGTGGCGGCGGAGCTTTTCAGAGGGGCTGGGAACTTCGACAGGCGAG 1500
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Db 15332 AAGTGTCCCTTTACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 15391
QY 1981 AGCTGCGGCTGAGTGCCA 2000
Db 15392 AGCTGCGGCTGAGTGCCA 15411

RESULT 4
AC116044
LOCUS
DEFINITION Papio hamadryas clone RP41-7017, *** SEQUENCING IN PROGRESS ***, 11 ordered pieces.
AC116044

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

AC116044.2 GI:42270667
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Papio hamadryas (hamadryas baboon)
Papio hamadryas
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.
1 (bases 1 to 175167)
Birren, B., Nusbaum, C. and Lander, E.
Papio hamadryas, Clone RP41-7017
Unpublished
2 (bases 1 to 175167)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K., Lamazares, R., Landers, T., Lehotzky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Sever, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodor, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 175167)

TITLE
JOURNAL
REFERENCE
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Sever, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodor, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (04-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 4, 2004 this sequence version replaced gi:19697483.
All repeats were identified using RepeatMasker.
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center Project name: U12529
Center clone name: 7_0_17

TITLE
JOURNAL
COMMENT

Submitted (04-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 4, 2004 this sequence version replaced gi:19697483.
All repeats were identified using RepeatMasker.
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center Project name: U12529
Center clone name: 7_0_17

7007 61:38 09 28 NOV TMS
- COPY -
0000 0000 0000 0000

143875	DB	TCTAATAAAGATTCTATAATAAGTACCAAGCTAGTGGTACCAATCTCGCAGAGT	143933
476	QY	CAGGCCTCTACCTGCTGATGACAAATGGCACACTATGCTTTTAACTGATTCAGACC	535
143935	DB	CAGGCCTCGCCTGCTGATGCCAAATGGACGCTGTGCTTTTAAACCGATTTCAGACC	143994
536	QY	ACAAATGTTTTGTGAATATTTTCCACAGGAAAAAACCAGAGTAGTCTCAAATCTCTATA	595
143995	DB	ACAAGTGTTTGTGAATATCTCCCTCCGCGGAAAAACAGAAGTAGTCTCAAATCTCTATA	144052
596	QY	CATCCATTATATTAGTTTTTACCTGTGATTTGGAAAAACCCAGACTCTGATTGCATTTTCAGG	655
144053	DB	CATCCATTAGCTTAGTTTTTACCTATGATTTGGAAAAACCCAGCTCTGATTGCATTTTCAGG	144112
656	QY	GCGGACAGGCTTTGGTGCACTCTCTGGCGGGATTTTCCATTTTAACTCCTTCTAGAAG	715
144113	DB	CCGGAGAGCCCTTTGGTGCACTGCTCTGGCGGGATTTTGCATTTTAACTCCTTCTGGAAG	144172
716	QY	CGCCTTCTCATGTTAAAGTTCCTGATGCCGCCAGGAGCGCCGAGGACAGGGCAGGGGCT	775
144173	DB	CGCCTTCTCATGTTAAAGTTCCTGATGCCGCCAGGAGCGCCGAGGGGAGGGCAAGGGCT	144232
776	QY	GGAGACGCCCCCGCAGAGGGCTACGTCGCTCTGGAACAGAGGTCCTCTGCTCCTCTCGCG	835
144233	DB	GCAGACGCCCCCGCAGAGGGCTACGCGCCTCTGCTGAAACAGGGGTCTCTGCTCCTCT	144289
836	QY	GCGCCAGCCCACTCCCAACAACCCCTCGCGGAGAAAGCCCCCAAGGGGAGGAGCGGGCT	895
144290	DB	GCGCCAACCCACTTCCCAACACCCCTGTGGAGAAAGCTTCAAGGGGAGGAGCGGGCT	144349

Qy	896	GGCCCTGCCCCGAGACCTTCGGTCTCTAGTTCGAGTCTGAATCGCCCTTGGACCCCT	955
Db	144350	GGCCCTGCCCTGAGCACCTTGGTCTCCAGGTC-----AATCGCCCTCGGACCCCT	144401
Qy	956	GCTTGGCTTCGGGACCCCTGCAGAGCTCCACAGGCGCCGTCGCCTCTCTCTCTGCT	1015
Db	144402	GCTTGGCTTCGGGACCCCTGCAGAGCTCCACAGGCGCCGTCGCCTCTCTCTCTGCT	144461

1016 TTTTATCCTCCCCAGACCTCTGGCAGGAACCGCTCATCGTTAC----- 1058

144462	CTTTTATCCTCCCGAGACTCTCGCAGGAA	CAATTGCTGGTTAAGCCCTTTCTCAGGTTA	144521
Qy			
144522	AGCCCTTTTCGACGCTCAGACCTCAGCGCTCAGCGCTCAGCTAGAGCGC	144581	
Db			
144582	GGCCCGGGGATGTGGCGGAGCTTCGCGCTCGCTGACCAATCGAATGTGGCGTCCATCG	144641	
Qy			
144642	ACTGGCGTGCSCCAGCGCAATTAGCAGCGCTCCCGCGCGCGTCCGCCGGCAACCC	144701	
Db			
144702	GGTGTGTGTGCTGCCGTGGAAACCGTGGCTAGCTGAGCTGAGGCTCTCGCTCCTGAGAG	144761	
Qy			
144762	GGTAAACTGCAACGCGCCACCGGCTATGCATGGGCTGGCGCCCTTGTGGGC----	144821	
Db			
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DEFINITION	Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCR12-GGT Region,		
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ACCESSION	AC002472		
VERSION	AC002472.8	GI:24137490	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 147086)		
REFERENCE	Budarf, M.L. and Emanuel, B.S.		
	Unpublished		
AUTHORS	2 (bases 1 to 147086)		
TITLE	Zhang, G., Zhan, M., Lao, V. and Roe, B.A.		
JOURNAL	Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCR12-GGT Region		
REFERENCE	3 (bases 1 to 147086)		
AUTHORS	Zhang, G., Lao, V., Zhan, M. and Roe, B.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-AUG-1997) Department Of Chemistry And Biochemistry,		
REFERENCE	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,		
	OK 73019, USA		
AUTHORS	4 (bases 1 to 147086)		
TITLE	Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (10-SEP-1998) Department Of Chemistry And Biochemistry,		
	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,		
AUTHORS	OK 73019, USA		
TITLE	5 (bases 1 to 147086)		
JOURNAL	Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.		
REFERENCE	Direct Submission		
	Submitted (23-OCT-1998) Department Of Chemistry And Biochemistry,		
AUTHORS	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,		
TITLE	OK 73019, USA		
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Location/Qualifiers
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Best Local Similarity 78.1%; Pred. No. 3.3e-262;
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DEFINITION
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sequence.
AC007664
AC007664.12 GI:5903121
VERSION

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KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 162470)
JOURNAL Zhan,M. and Roe,B.A.
AUTHORS Homo sapiens 22q11 BAC Clone b453h4 In The BCR12-GGT Region
TITLE 2 (bases 1 to 162470)
JOURNAL Unpublished
AUTHORS Zhan,M. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 162470)
AUTHORS Zhan,M. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 4 (bases 1 to 162470)
AUTHORS Zhan,M. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 5 (bases 1 to 162470)
AUTHORS Zhan,M. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 6 (bases 1 to 162470)
AUTHORS Zhan,M. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Sep 18, 1999 this sequence version replaced gi:5882763.
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Best Local Similarity 78.1%; Pred. No. 3.3e-262;
Matches 1446; Conservative 0; Mismatches 236; Indels 169; Gaps 11;
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DEFINITION Sequence 8830 from Patent WO0157278.
ACCESSION CQ073030
VERSION CQ073030.1 GI:41042899

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human cells or other human cervical epithelial cells
JOURNAL Patent: WO 0157278-A 8830 09-AUG-2001;
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Best Local Similarity 100.0%; Pred. No. 4.8e-139;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 12704 from Patent WO0157272.
ACCESSION CQ103845
VERSION CQ103845.1 GI:41072896

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 12704 09-AUG-2001;
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Best Local Similarity 100.0%; Pred. No. 4.8e-139;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 CACTGAAAGCTGGGTGACAGAGCAAGACCTGGCTCTTAATAATGAATACATAAAGTCTC 445
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 DEFINITION Sequence 12677 from Patent WO0157276.
 ACCESSION Q142655
 VERSION Q142655.1 GI:41100027
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 Human genome-derived single exon nucleic acid probes useful for
 analysis of gene expression in human bone marrow
 Patent: WO 0157276-A 12677 09-AUG-2001;
 Aeonica, Inc. (US)
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QY 386 CACTGAAAGCTGGGTGACAGAGCAAGACCCCTGGCTCTAATAAATGAATACATAAAGTCTC 445
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 Human genome-derived single exon nucleic acid probes useful for
 analysis of gene expression in human heart
 Patent: WO 0157274-A 9542 09-AUG-2001;
 Aeonica, Inc. (US)
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 Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION CQ225890.1 GI:41208950
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 SOURCE Homo sapiens
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 REFERENCE
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
 JOURNAL Molecular Dynamics Sequence Listing Engine
 Patent: WO 0157273-A 12729 09-AUG-2001;
 Aeomica, Inc. (US)
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 DEFINITION Sequence 12201 from Patent WO0157277.
 ACCESSION CQ263940
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 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 REFERENCE
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver
 Patent: WO 0157277-A 12201 09-AUG-2001;
 Aeomica, Inc. (US)
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 Best Local Similarity 100.0%; Pred. No. 4.8e-139;
 Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 503 ACAGTATGCTGTTAACTGATGACAGCAAAATGTTTGTGAATATTTTCCCGAGG 444
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QY      746  CCAGGAGCGCGAGGAGAGCGGGGCTGAGAGCGCCCGCAGAGGCTACGTGCCCT 805
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VERSION    CQ301025.1 GI:41261602
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

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REFERENCE
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL     Patent: WO 0186003-A 12130 15-NOV-2001;
            Aecomica, Inc. (US)
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Query Match      28.1%; Score 563; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 4.8e-139;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 12395 from Patent WO0157275.
ACCESSION CQ338301
VERSION    CQ338301.1 GI:41287372
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

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REFERENCE
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human brain
JOURNAL     Patent: WO 0157275-A 12395 09-AUG-2001;
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Best Local Similarity 100.0%; Pred. No. 4.8e-139;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	83	GAGAAAGCCCCAAGGGAGGAGACGGGCTGCCCCCTGCCCGAGCACCTTCGGTCTCTA	24
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 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Penn, S. G., Hanzel, D. K., Chen, W. and Rank, D. R.
 Human genome-derived single exon nucleic acid probes useful for
 analysis of gene expression in human placenta
 Patent: WO 0157272-A 12598 09-AUG-2001;
 Aecomica, Inc. (US)
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GenCore version 5.1.6
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C 9	448.8	22.4	498	6	CD637540 56017465H
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C 40	135.8	6.8	383	6	CA396428
C 41	130.2	6.5	2945	3	BC028231
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DEFINITION full-length cDNA clone CS0DI033YM19 of Placentia Cot 25-normalized
of Homo sapiens (human).

ACCESSION CR622747 GI:50503554
VERSION CR622747.1
KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1678)
Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;
Eukaryota; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Li W.B., Gruber C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

REFERENCE 2 (bases 1 to 1678)
Genoscope.

AUTHORS Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES Location/Qualifiers

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ORIGIN

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DB 514 TCCCTGTGATTGGGAAAACCCAGCTCTGATTGATTTTCAGGGCGGGACAGCTTTGTG 455

674 CACTGTCTGGCGGATTTTCAATTTAACTCTCTTAGAAGCGCTTCTCATGTAAAG 733
 454 CACTGTCTGGCGGATTTTCAATTTAACTCTCTTAGAAGCGCTTCTCATGTAAAG 395
 734 TTCTGATGTCGGCGGAGCGCGAGAGAGCGGCGCTGAGAGCGCGCGGAGAGG 793
 394 TTCTGATGTCGGCGGAGCGCGAGAGAGCGGCGCTGAGAGCGCGCGGAGAGG 335
 794 GCTACGTGCTCTGCTGAGACAGAGTCTCTGCTCTCTCGCGCGCGCGACCTCCCA 853
 334 GCTACGTGCTCTGCTGAGACAGAGTCTCTGCTCTCTCGCGCGCGCGACCTCCCA 275
 854 CAACCCCTGGCGGAGAGCGCGCGAGAGAGCGGCGCTGAGAGCGCGCGGAGAGG 913
 274 CAACCCCTGGCGGAGAGCGCGCGAGAGAGCGGCGCTGAGAGCGCGCGGAGAGG 215
 914 CTTCCGTCTCTAGTCTGGAGTCTGAATCGGCTTGGGACCGCTTGGCTTGGGAGCC 973
 214 CTTCCGTCTCTAGTCTGGAGTCTGAATCGGCTTGGGACCGCTTGGCTTGGGAGCC 155
 974 CTGCAAGAGTCTACAGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1033
 154 CTGCAAGAGTCTACAGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 95
 1034 TCTGGCAGGACCGCTCATGCTAGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 1093
 94 TCTGGCAGGACCGCTCATGCTAGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 35
 1094 CGTTGGCGCTCTCACTTAGAGCGCGACCGGGGA 1127
 34 CGTTGGCGCTCTCACTTAGAGCGCGACCGGGGA 1

RESULT 2

BI668929/c
 LOCUS 603294907F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314345 5',
 DEFINITION mRNA sequence.
 ACCESSION BI668929
 VERSION BI668929.1 GI:15583162
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11796 Row: m Column: 02
 High quality sequence stop: 758.
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 /lab_host="DH10B"
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 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN

Query Match 24.6%; Score 492.2; DB 4; Length 760;
 Best Local Similarity 99.2%; Pred. No. 1.6e-104;
 Matches 505; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 615 ACCTGTGATTTGGGAAACCCAGCTCTGATTTGATTTTCAGGGCGGAGACGCTTTGGTGC 674
 Db 517 ATCTGTGATTTGGGAAACCCAGCTCTGATTTGATTTTCAGGGCGGAGACGCTTTGGTGC 458
 QY 675 ACTGTCTGGCGGATTTTCAATTTAACTCTCTTAGAAGCGCTTCTCATGTAAAGT 734
 Db 457 ACTGTCTGGCGGATTTTCAATTTAACTCTCTTAGAAGCGCTTCTCATGTAAAGT 398
 QY 735 TCCTGATGTCGGCGGAGAGCGCGAGAGAGCGGCGCTGAGAGCGCGCGGAGAGG 794
 Db 397 TCCTGATGTCGGCGGAGAGCGCGAGAGAGCGGCGCTGAGAGCGCGCGGAGAGG 338
 QY 795 CTAGTGTCTCTGCTGAGAGAGTCTCTGCTCTCTGCGGCGGCGAGCCCTCCAC 854
 Db 337 CTAGTGTCTCTGCTGAGAGAGTCTCTGCTCTCTGCGGCGGCGAGCCCTCCAC 278
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 Db 277 AACCCCTGCGGAGAGAGCGCGAGAGAGCGGCGCTGAGAGCGCGCGGAGAGG 218
 QY 915 TTCCGTCTCTGATGTCGGAGTCTGAATCGGCGCTTGGGACCGCTTGGCTTGGGGA-CCC 973
 Db 217 TTCCGTCTCTGATGTCGGAGTCTGAATCGGCGCTTGGGACCGCTTGGCTTGGGGA-CCC 158
 QY 974 CTGCAAGAGTCTACAGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1033
 Db 157 CTGCAAGAGTCTACAGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 98
 QY 1034 TCTGGCAGGACCGCTCATGCTAGCGCGCGCTTTCAGAGCGCTCAGACCTCAGCGGAGAG 1093
 Db 97 TCTGGCAGGACCGCTCATGCTAGCGCGCGCTTTCAGAGCGCTCAGACCTCAGCGGAGAG 38
 QY 1094 CGTTGGCGCTCTCACTTAGAGCGCGAGCC 1122
 Db 37 CGTTGGCGCTCTCACTTAGAGCGCGAGCC 9

RESULT 3

BI668929/c
 LOCUS BX336850/2
 DEFINITION BX336850 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI033YM19 5-PRIME, mRNA sequence.
 ACCESSION BX336850
 VERSION BX336850.2 GI:46267442
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 841)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 2, 2003 this sequence version replaced gi:30333549.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10362.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI033AG10QP1&c=10362.r.

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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 24.6%; Score 491.8; DB 5; Length 841;
Best Local Similarity 99.4%; Pred. No. 2.1e-104;
Matches 504; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 614 TACCTGTGGATTGGGAAACCCAGCTCTGATTCATTTTCAGGCGGAGAGCCTTTGGTG 673
Db 515 TGCTGTGGATTGGGAAACCCAGCTCTGATTCATTTTCAGGCGGAGAGCCTTTGGTG 456
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Qy 734 TTCTGTATGCGGCGGAGGCGGAGAGGAGGCGGAGGAGGCGGAGGAGGCGGAGGAGG 793
Db 395 TTCTGTATGCGGCGGAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 336
Qy 794 GCTACGTGCGCTGTGACAGAGGTCTCTGCTCTCTGAGAGCGCTTCTCATGGTAAAG 853
Db 335 GCTACGTGCGCTGTGACAGAGGTCTCTGCTCTCTGAGAGCGCTTCTCATGGTAAAG 276
Qy 854 CAACTCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 913
Db 275 CAA-CCCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 217
Qy 914 CTTCCGCTCTAGTTCGAGTCTGAATCGGCTTGGGAGCCTCTGCTGCTTGGGAGCCT 973
Db 216 CTTCCGCTCTAGTTCGAGTCTGAATCGGCTTGGGAGCCTCTGCTGCTTGGGAGCCT 157
Qy 974 CTGCAAGAGCTGACAGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1033
Db 156 CTGCAAGAGCTGACAGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 97
Qy 1034 TCTGCGAGGAGCCTCATCGTTACGCGCCCTTTTCGAGCCTTCAGACCTTCAGGCGGAGAC 1093
Db 96 TCTGCGAGGAGCCTCATCGTTACGCGCCCTTTTCGAGCCTTCAGACCTTCAGGCGGAGAC 37
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RESULT 4
CN368433/c
LOCUS
DEFINITION 17000600187603 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN368433
VERSION CN368433.1 GI:47368367
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 743)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.
TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 743 Std Error: 0.00.

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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="GRN_PREHEP"
/note="oligo dT primed, full-length enriched cDNA library from DMSO-treated H9 cell line H9 (p22) maintained in feeder-free conditions"

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Query Match 24.2%; Score 483.4; DB 7; Length 743;
Best Local Similarity 99.8%; Pred. No. 1.9e-102;
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 675 ACTGCTCTGCGGAGTTTTCATTTTAACCTCTCTAGAGCGCTTCTCATGGTAAAGT 734
Db 425 ACTGCTCTGCGGAGTTTTCATTTTAACCTCTCTAGAGCGCTTCTCATGGTAAAGT 366
Qy 735 TCTCATGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 794
Db 365 TCTCATGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 306
Qy 795 CTACGTCGCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 854
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Db 245 AACCCCTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 186
Qy 915 TTCCGCTCTAGTTCGAGTCTGATTCGCGCTTGGGAGCCTCTGCTTGGGAGCCTCT 974
Db 185 TTCCGCTCTAGTTCGAGTCTGATTCGCGCTTGGGAGCCTCTGCTTGGGAGCCTCT 126
Qy 975 TGCAGAGAGCTCCACAGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1034
Db 125 TGCAGAGAGCTCCACAGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 66
Qy 1035 CTGCGAGAGAACCGCTCATCGTTACGCCCTTTTCGAGCCTTCAGACCTTCAGGCGGAGAC 1094
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Qy 1095 GCTTGT 1099
Db 5 GCTTGT 1

RESULT 5
CD637541
LOCUS
DEFINITION 56017465J1 FLP Homo sapiens cDNA, mRNA sequence.
EST 663 bp
mRNA linear
EST 12-JAN-2004

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ACCESSION	CD637541				
VERSION	CD637541.1	GI:40285552			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.				
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput				
COMMENT	extension cloning of partial genes				
	Genomics 84 (1), 203-210 (2004)				
	Contact: Fu GK				
	Incyte Genomics, Inc.				
	3160 Porter Dr., Palo Alto, CA 94304, USA				
	Tel: 6508454102				
	Email: gfu@incyte.com.				
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	/clone_lib="PLP"				
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	Best Local Similarity 99.0%; Pred. No. 1.2e-101;				
	Matches 483; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
Qy	614 TACCTGTGGATTGGGAAACCACACTCTGATTTGCATTTTCAGGGCGGACAGCCTTTGGTG	673			
Dd					
Qy	166 TGCCTGTGGATTGGGAAACCACACTCTGATTTGCATTTTCAGGGCGGACAGCCTTTGGTG	225			
Dd					
Qy	674 CACTGTCTGGCGGATTTTCCATTTTAACCTCTCTAGAAGCGCCTTCTCATGTGTAAG	733			
Dd					
Qy	226 CACTGCTCTGGCGGATTTTCCATTTTAACCTCTCTAGAAGCGCCTTCTCATGTGTAAG	285			
Dd					
Qy	734 TTCTGTATGCCGACAGAGCGCCGAGAGAGGGCAGGGGCTGGAGACGCCCGCAGAGG	793			
Dd					
Qy	286 TTCCTATGCCGACAGAGCGCCGAGAGAGGGCAGGGGCTGGAGACGCCCGCAGAGG	345			
Dd					
Qy	794 GCTACGTGCCCTCTGTGACAGAGGTCTTCCTGCCTCTCGGGCGCCAGGCCACCTCCCA	853			
Dd					
Qy	346 GCTACGTGCCCTCTGTGACAGAGGTCTTCCTGCCTCTCGGGCGCCAGGCCACCTCCCA	405			
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Qy	854 CAACCCCTCGGGAGGAAGCCCCAAGGGAGGAGACGGGCTGGCCCTGCCCGCAGCAC	913			
Dd					
Qy	406 CAACCCCTCGGGAGAGACCCCCAAGGGAGGAGACGGGCTGGCCCTGCCCGCAGCAC	465			
Dd					
Qy	914 CTTCGGTCTTAGTGGAGTCTGAATCGGCCTTGGACCTCTGTTGGCTTCGGGGACCC	973			
Dd					
Qy	466 CTTCGGTCTTAGTGGAGTCTGAATCGGCCTTGGACCTCTGTTGGCTTCGGGGACCC	525			
Dd					
Qy	974 CTCGAGAGCTCACAGGCGCGTCCCTCTTCCTCTCTCTCTTTTATCTCTCCGAGACC	1033			
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Qy	526 CTCGAGAGCTCACAGGCGCGTCCCTCTTCCTCTCTCTCTTTTATCTCTCCGAGACC	585			
Dd					
Qy	1034 TCTGGCAGGAACCGCTCATCGTTACGCCCTTTTCGAGCCTTCAGACCTTCGAGCGGAGAC	1093			
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Qy	586 TCTGGCAGGAACCGCTCATCGTTACGCCCTTTTCGAGCCTTCAGACCTTCGAGCGGAGAC	645			
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Qy	1094 CGCTTGGC 1101				
Dd					
Qy	646 CGTTGGGC 653				
Dd					

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Fu.G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
JOURNAL Circular rapid amplification of cDNA ends for high-throughput
COMMENT extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES source
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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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Best Local Similarity 99.6%; Pred. No. 1.3e-101;
Matches 481; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	614	TACTGTGTGATTGGGAAAACCCAGCTCTGATTGCATTTTCAGGCGGGACAGCCTTTGGTG	673
Db	483	TGCGCTGTGATTGGGAAAACCCAGCTCTGATTGCATTTTCAGGCGGGACAGCCTTTGGTG	424
Qy	674	CACCTGTCTGCGGGATTTTCCTATTTTAACTCTCTTAGAAGCGCCTTCTCATGGTAAAG	733
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Qy	734	TTCTTGATCCGCCAGGAGCGCCAGGAGAGGCGAGGGCTGTGAGACGCCCGCAGAGG	793
Db	363	TTCTTGATCCGCCAGGAGCGCCAGGAGAGGCGAGGGCTGTGAGACGCCCGCAGAGG	304
Qy	794	GCTACGTGCGCTGCTGGACAGAGGTCTCTGCTCTCTCGCGCGCGGAGCCCACTTCCCA	853
Db	303	GCTACGTGCGCTGCTGGACAGAGGTCTCTGCTCTCTCGCGCGCGGAGCCCACTTCCCA	244
Qy	854	CAACCCCTCGGGAGAAAGCCCAAGCGGAGGAGACGGCCTTGGCCCTTGCCTCCGAGCAC	913
Db	243	CAACCCCTCGGGAGAAAGCCCAAGCGGAGGAGACGGCCTTGGCCCTTGCCTCCGAGCAC	184
Qy	914	CTTCCGTCTCTAGGTCGGAGTCTGAATCGGCCCTTGGGACCCCTGCTTGGGTCGGGACCC	973
Db	183	CTTCCGTCTCTAGGTCGGAGTCTGAATCGGCCCTTGGGACCCCTGCTTGGGTCGGGACCC	124
Qy	974	CTGCAAGAGCTGCACAGGCGCGGTCGCTCTTCTCTCTGCTTTTATCTCTCCCAAGACC	1033
Db	123	CTGCAAGAGCTGCACAGGCGCGGTCGCTCTTCTCTCTGCTTTTATCTCTCCCAAGACC	64
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Db	3	CGC 1	

RESULT 6
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LOCUS
DEFINITION
CD637276
ACCESSION
CD637276.1
VERSION
GI:40285543

651 bp mRNA linear
56017301h1 FLP Homo sapiens cDNA, mRNA sequence.

EST 12-JAN-2004

RESULT 7	CD637277	CD637277	CD637277	652 bp	mrna	linear	EST 12-JAN-2004
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DEFINITION	CD637277						
ACCESSION	CD637277.1	GI:40285544					
VERSION	EST						
KEYWORDS	EST						
SOURCE	Homo sapiens (human)						


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ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 662)
AUTHORS      Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE        Circular rapid amplification of cDNA ends for high-throughput
               extension cloning of partial genes
JOURNAL       Genomics 84 (1), 205-210 (2004)
COMMENT      Contact: Fu GK
               Incyte Genomics, Inc.
               3160 Porter Dr., Palo Alto, CA 94304, USA
               Tel: 6509454102
               Email: gfu@incyte.com.
FEATURES     Location/Qualifiers
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Db	166	TGCTGTGGATTGGGAAAACCCAGCTCTGATTGCAATTCAGGGCGGACAGCCTTTGGTG	225	
Qy	674	CACGTGCTGGCGGATTTTCCATTTTAACTTCCTTCTAGAGCGCCTTCTCATGTATAAG	733	
Db	226	CACGTGCTGGCGGATTTTCCATTTTAACTTCCTTCTAGAGCGCCTTCTCATGTATAAG	285	
Qy	734	TTCCTGATCCGCCAGAGAGCGCCAGAGAGAGGGCAGGGGCTGGAGACGCCCCGACAGG	793	
Db	286	TTCCTGATCCGCCAGAGAGCGCCAGAGAGAGGGCAGGGGCTGGAGACGCCCCGACAGG	345	
Qy	794	GCTACGTGCCCTGCTGGACAGAGTCTCTGCTCCTTCGGGGGGCCAGGCCCACTCCCA	853	
Db	346	GCTACGTGCCCTGCTGGACAGAGTCTCTGCTCCTTCGGGGGGCCAGGCCCACTCCCA	405	
Qy	854	CAACCCCTCGGGAGAACGCCCCCAAGGGGAGAGACGGGCTGCGCCCTGCCCCGAGCAC	913	
Db	406	CAACCCCTCGGGAGAACGCCCCCAAGGGGAGAGACGGGCTGCGCCCTGCCCCGAGCAC	465	
Qy	914	CTTCGCTCTTAGTTCGAGTCTGAATCGGCTTTGGACCTGCTGGCTTCGGGGACCC	973	
Db	466	CTTCGCTCTTAGTTCGAGTCTGAATCGGCTTTGGACCTGCTGGCTTCGGGGACCC	525	
Qy	974	CTGCAAGACGTCACAGCGCGCTGCGCTCTTCCTCTGCTTTTTTATCTCTCCCGACAC	1033	
Db	526	CTGCAAGACGTCACAGCGCGCTGCGCTCTTCCTCTGCTTTTTTATCTCTCCCGACAC	585	
Qy	1034	TCTGGCAGGAACCGCTCATCGTTACGCCCTTTCGCAGCCTCAGACCTGAGCGGAGAC	1093	
Db	586	TCTGGCAGGAACCGCTCATCGTTATGCCCTTTCGCAGCCTCAGA-CTGAGCGGAGAC	644	
Qy	1094	CGTTGGC 1101		
Db	645	CGTTGGC 652		

RESULT 8
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CN368432 596 bp mRNA linear EST 16-MAY-2004
DEFINITION
17000424376481 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION
CN368432
VERSION
CN368432.1 GI:47368366
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 586) Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.		
TITLE	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation		
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)		
COMMENT	Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert length: 586 Std Error: 0.00.		
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DEFINITION	56017465H1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD637540		
VERSION	CD637540.1	GI:40285551	
KEYWORDS	EST.		

RESULT 9	CD637540/c	498 bp	linear	EST 12-JAN-2004
LOCUS	CD637540		mrna	
DEFINITION	56017465H1 FLP Homo sapiens cdna, mRNA sequence.			
ACCESSION	CD637540			
VERSION	CD637540.1			
KEYWORDS	GI:40285551			
	EST.			

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 498)
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)
 COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com
 FEATURES
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 /clone_lib="FLP"
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 Db 304 GGCTACGTCTGCTGTGACAGAGTCTCTGCTCTCTGCGCGGCGGCGGCGGCGG 245
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 Db 124 CTTGCAAGACGTCACAGGCGCGCTGCGCTCTTCTCTCTCTTTTATCTTCCCGAGAC 65
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 Homo sapiens cDNA clone hd01g10 5', mRNA sequence.
 ACCESSION BQ635907
 VERSION BQ635907.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 646)
 AUTHORS Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
 TITLE Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
 JOURNAL Mol. Vis. 8 (4), 196-204 (2002)
 COMMENT 22103461
 PUBLISHED 12107411
 COMMENT Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 01 row: g column: 10
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers
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 /notes="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library in the construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor
 [5'-PGACTAGTCTTAGATCGGAGCGGCGGCTT)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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 Best Local Similarity 99.8%; Pred. No. 5.3e-94;
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Db	263	GCTACGTGCCCTCTGGACAGAGGTCTCTGCTCTCTCGCGCGCGCCAGAGCCACCTCCCA	204
Qy	854	CACACCCCTGGCGGAGAGCCGCCAGAGGGAGGAGACGGGGCTCTGGCCCTGCCCCGAGCAC	913
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Db	143	CTTTCGGTCTCTAGGTCGGACTCTGAATCGGCCCTGGGACCTGTGGCTTCGGGGACCC	84
Qy	974	CTCAAGAAGTCACAGCGCGTGCTCTTTCTCCTCTGTTTTTATCTCCCCA-GAC	1032
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LOCUS					

DEFINITION 17000424702964 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN368430

VERSION CN368430.1 GI:47368364
KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Craniata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 689)
AUTHORS
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,

Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.

TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R

Regenerative Medicine
Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA
Tel.: 650 473 8658

Tel: 650 473 0050
 Fax: 650 473 7760
 Email: thbrandenberger@acron.com

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ORIGIN

and H9 (p26) maintained in feeder-free conditions"

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QY 794 GCTACGTGCGCTGCTGGACAGAGGTCTCTGCGCTCGGCGCGGCGGCGGCGGCGGCGGCGG 853
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VERSION CD637543.1 GI:40285554
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 574)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: sfu@incyte.com
Location/Qualifiers
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QY 794 GCTACGTGCGCTGCTGGACAGAGTCTCTGCGCTCTGCGGCGGCGGCGGCGGCGGCGGCGG 853
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Search completed: November 21, 2004, 17:35:08
Job time : 6410.8 secs

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Ddb	61	TATAGCCACCTGCCTCCTCCCTGCCTGCCTGCATCACTACCTGCCTATTTTTGGCTCTAG	120		
QY	121	AAGCACTGCTTCTATGCTTCCTTAGGACCACTGCCCGCATATGACAGATAAGAACATCGA	180		
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SUMMARY

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3	1902.2	95.1	1938	13	US-10-027-632-98170		Sequence 98170, A
4	1902.2	95.1	1938	15	US-10-027-632-98169		Sequence 98169, A
5	1902.2	95.1	1938	15	US-10-027-632-98170		Sequence 98170, A
6	597.6	29.9	598	13	US-10-027-632-41182		Sequence 41182, A
7	597.6	29.9	598	15	US-10-027-632-41182		Sequence 41182, A
8	563	28.1	563	9	US-09-864-761-9542		Sequence 9542, Ap
9	554	27.7	554	9	US-09-864-761-9446		Sequence 9446, Ap
10	458.4	28.9	1904	15	US-10-094-749-1376		Sequence 1376, Ap
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Db ACCTGGCAACATACGAGATAAATAATTTAAATTTAGCCAGATGTGATCCCGCTG 300
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1981 AGCTGGGCTGACGCTGCCA 2000
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RESULT 2

US-10-027-632-98169
; Sequence 98169, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363


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; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
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US-10-027-632-98169

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Query Match	95.1%	Score	1902.2	DB	13	Length	1938
Best Local Similarity	99.9%	Pred.	No.	0			
Matches	1901	Conservative	2	Mismatches	0	Indels	0
QY	1	TC	CC	AA	GT	CC	AT
DB	36	TC	CC	AA	GT	CC	AT
QY	61	TAT	AG	CC	AC	CT	GC
DB	96	TAT	AG	CC	AC	CT	GC
QY	121	AAG	CA	CT	GC	TC	CT
DB	156	AAG	CA	CT	GC	TC	CT
QY	181	GG	CT	AA	GC	CA	AA
DB	216	GG	CT	AA	GC	CA	AA
QY	241	AC	CT	GG	CA	AC	TA
DB	276	AC	CT	GG	CA	AC	TA
QY	301	TAG	CT	C	AG	CA	CT
DB	336	TAG	CT	C	AG	CA	CT
QY	361	GC	AG	CT	AG	CT	AG
DB	396	GC	AG	CT	AG	CT	AG
QY	421	CT	AA	TA	AG	CT	AA
DB	456	CT	AA	TA	AG	CT	AA
QY	481	CT	CT	AC	CT	GC	TA
DB	516	CT	CT	AC	CT	GC	TA
QY	541	TC	TT	TT	GT	GA	TA
DB	576	TC	TT	TT	GT	GA	TA
QY	601	AT	TA	TA	TA	TA	TA
DB	636	AT	TA	TA	TA	TA	TA
QY	661	AC	AG	CT	TT	GT	GC
DB	696	AC	AG	CT	TT	GT	GC
QY	721	TC	CT	AT	GT	GA	TA
DB	756	TC	CT	AT	GT	GA	TA
QY	781	GC	CC	CC	GC	AG	GC
DB	816	GC	CC	CC	GC	AG	GC

Qy	841	AGCCACGCTCCCAACACCCCTGTCGGGAGAAAGCCCCAAGGGGAGGAGACGGGCTCG3CCC	900
Db	876	AGCCACGCTCCCAACACCCCTGTCGGGAGAAAGCCCCAAGGGGAGGAGACGGGCTCG3CCC	935
Qy	901	CTGCCCGAGACACTTCCGTCCTAGGTCGGAGCTCGAATCGCGCTTGGACGCTCGCTTG	960
Db	936	CTGCCCGAGACACTTCCGTCCTAGGTCGGAGCTCGAATCGCGCTTGGACGCTCGCTTG	995
Qy	961	GCTTCGGGGACCCCTGCAAGACGTCACAGGCGCGCGTCGCTTCTCTCTCTCTTTTAA	1020
Db	996	GCTTCGGGGACCCCTGCAAGACGTCACAGGCGCGCGTCGCTTCTCTCTCTCTTTTAA	1055
Qy	1021	TCTCTCCCGACACTCTGGCAGGAACCGCTCATGTTACGCCCTTTTCGACGCTCAGACC	1080
Db	1056	TCTCTCCCGACACTCTGGCAGGAACCGCTCATGTTACGCCCTTTTCGACGCTCAGACC	1115
Qy	1081	CTGAGCGGAGACCGCTTGGCGCTCACTTAGAGCGGACCCGGGATCTGGGCGAGTC	1140
Db	1116	CTGAGCGGAGACCGCTTGGCGCTCACTTAGAGCGGACCCGGGATCTGGGCGAGTC	1175
Qy	1141	TGCGGCTGCGCTGACCAATCGAGTGTGGCGTCCATCGACTGGCTGTGCAAGGCAATTA	1200
Db	1176	TGCGGCTGCGCTGACCAATCGAGTGTGGCGTCCATCGACTGGCTGTGCAAGGCAATTA	1235
Qy	1201	GCAGCGCTCCCCCGCGCGTTCGCCCGGCAACCCAGTCTGTAGGTTGCGTAGAAA	1260
Db	1236	GCAGCGCTCCCCCGCGCGTTCGCCCGGCAACCCAGTCTGTAGGTTGCGTAGAAA	1295
Qy	1261	CGTGGCTCTCTGCGCTGAGGCTCTCGCCTGAGAGGATAAATGCACGCCACCGGC	1320
Db	1296	CGTGGCTCTCTGCGCTGAGGCTCTCGCCTGAGAGGATAAATGCACGCCACCGGC	1355
Qy	1321	TATGCACTGGGCTGGCGCTTGTGGGATCTCTCGCTGCCCTTCCTAGGGGTTCCAGCAT	1380
Db	1356	TATGCACTGGGCTGGCGCTTGTGGGATCTCTCGCTGCCCTTCCTAGGGGTTCCAGCAT	1415
Qy	1381	CGCCCCCTTTCGTGGACTGGGAAACAGCCTGACTCCAGAGACTTGTGTTCCTCACATG	1440
Db	1416	CGCCCCCTTTCGTGGACTGGGAAACAGCCTGACTCCAGAGACTTGTGTTCCTCACATG	1475
Qy	1441	CACTGGGAGAGTGGCGGGGGCAGCTTTTCAGAGGGCTGGGAACTTCGACAGCCAG	1500
Db	1476	CACTGGGAGAGTGGCGGGGGCAGCTTTTCAGAGGGCTGGGAACTTCGACAGCCAG	1535
Qy	1501	GTCACTCTCACTCTGTGCCCTTAGTTATCTTCGATGCTCTGCTTTCGATACGCTG	1560
Db	1536	GTCACTCTCACTCTGTGCCCTTAGTTATCTTCGATGCTCTGCTTTCGATACGCTG	1595
Qy	1561	CTCCCTGCACAGGAACCTCCATCCCCATCTTGTCTGCTTGTGGAATCTCAGAAATCTG	1620
Db	1596	CTCCCTGCACAGGAACCTCCATCCCCATCTTGTCTGCTTGTGGAATCTCAGAAATCTG	1655
Qy	1621	CAAGGTCAGCTTAGAGTCACTTCTTCGGAAGCTTTTCCTCAACACCTCTCCGCGCTG	1680
Db	1656	CAAGGTCAGCTTAGAGTCACTTCTTCGGAAGCTTTTCCTCAACACCTCTCCGCGCTG	1715
Qy	1681	CTGTGCTGCCCTCAGGCGCTCTCTCACAGCACTGATAACAGGTGTCCGCTCTCCACCT	1740
Db	1716	CTGTGCTGCCCTCAGGCGCTCTCTCACAGCACTGATAACAGGTGTCCGCTCTCCACCT	1775
Qy	1741	CCACCACTCCACTCCACCCCAAGGAGTGAAGCCAGAGGCGAGGACAGAGTCTGTC	1800
Db	1776	CCACCACTCCACTCCACCCCAAGGAGTGAAGCCAGAGGCGAGGACAGAGTCTGTC	1835
Qy	1801	TGTTCTCTGTGTCAGGCGCCACGAAGGAAATGTAGGAGGTTGGAGGTGAGGGCA	1860
Db	1836	TGTTCTCTGTGTCAGGCGCCACGAAGGAAATGTAGGAGGTTGGAGGTGAGGGCA	1895
Qy	1861	GCTGGGATAGGGTTGAGGGCTGGGTTGTGGAGGCTGGATCT	1903
Db	1896	GCTGGGATAGGGTTGAGGGCTGGGTTGTGGAGGCTGGATCT	1938

RESULT 3

US-10-027-632-98170
: Sequence 98170. Application US/10027632

US-10-027-632-98170
: Sequence 98170. Application US/10027632

Sequence 2019, Application No. US20020198371A1

: GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

FILE REFERENCE: 10027, 123
CURRENT APPLICATION NUMBER: US/10/027, 632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

; PRIOR FILING DATE: 2000-03-23
 ; PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: 03-8
PRIOR FILING DATE: 2000-02-24

; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363

;; PRIOR APPLICATION NUMBER: US 8
: PRIOR FILING DATE: 1999-11-23

; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358

;; PRIOR APPLICATION NUMBER: US 60/136,338
;; PRIOR FILING DATE: 1999-09-28

;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002

;; PRIOR APPLICATION NUMBER: US 6
; PRIOR FILING DATE: 1988-08-09

; PRIOR FILING DATE: 1999-08-09
 NUMBER OF SEQ ID NOS: 325730

; NUMBER OF SEQ ID NOS: 325/20
; COMMENT: FASTSEQ for Windows Version 4.0

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; SOFTWARE: Fast.
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; SEQ ID NO 9817

; LENGTH: 1938

; TYPE: DNA

	ORGANISM:	Human
1.	100	100
2.	98	98
3.	96	96
4.	94	94
5.	92	92
6.	90	90
7.	88	88
8.	86	86
9.	84	84
10.	82	82
11.	80	80
12.	78	78
13.	76	76
14.	74	74
15.	72	72
16.	70	70
17.	68	68
18.	66	66
19.	64	64
20.	62	62
21.	60	60
22.	58	58
23.	56	56
24.	54	54
25.	52	52
26.	50	50
27.	48	48
28.	46	46
29.	44	44
30.	42	42
31.	40	40
32.	38	38
33.	36	36
34.	34	34
35.	32	32
36.	30	30
37.	28	28
38.	26	26
39.	24	24
40.	22	22
41.	20	20
42.	18	18
43.	16	16
44.	14	14
45.	12	12
46.	10	10
47.	8	8
48.	6	6
49.	4	4
50.	2	2
51.	0	0

Query Match 95.1%; Score 1902.2; DB 13; Length 1938;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1901: Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCTCAAGTCNATGGGTCCCTGGTAGAGACAGGGGATGAATGTGAACCCCTGTCATGGC	60
Db	36	TCTCCAAGTCCATGGGTCCCTGGTAGAGACAGGGGATGAATGTGAACCCCTGTCATGGC	95
Qy	61	TATAGCCACTGCCTTCCTCCCTCCCTCGCATCACTACCTGGCCTATTTTTGGCCTTAG	120
Db	96	TATAGCCACTGCCTTCCTCCCTCCCTCGCATCACTACCTGGCCTATTTTTGGCCTTAG	155
Qy	121	AAGCACTGCTTCCTATGCTCCTTAGGACCACTGCCGCATATGACAGATAAAGAACATCGA	180
Db	156	AAGCACTGCTTCCTATGCTCCTTAGGACCACTGCCGCATATGACAGATAAAGAACATCGA	215
Qy	181	GGCTAAGGCAAGCGAAATCTTTTCTTAAAGTCATACAGCTGTCAAAAAGAAAGCTGGACA	240
Db	216	GGCTAAGGCAAGCGAAATCTTTTCTTAAAGTCATACAGCTGTCAAAAAGAAAGCTGGACA	275
Qy	241	ACCTGGGCAACATACGAGATAA AAAATATTATTAATTAGCAGATGTGGTAGCCCCCTG	300
Db	276	ACCTGGGCAACATACGAGATAA AAAATATTATTAATTAGCAGATGTGGTAGCCCCCTG	335
Qy	301	TAGTCTCAGCGACTCAGAGGCTGAGGAGAGGCTCACACAGAGTCGACAGATTCAAGAT	360
Db	336	TAGTCTCAGCGACTCAGAGGCTGAGGAGAGGCTCACACAGAGTCGACAGATTCAAGAT	395
Qy	361	GCAGTAGGCTATGATCCTGCCACTGCCACTGAAAGCTGGGTGA CAGAGCAAGACCTCGGCT	420
Db	396	GCAGTAGGCTATGATCCTGCCACTGCCACTGAAAGCTGGGTGA CAGAGCAAGACCTCGGCT	455
Qy	421	CTAATAAATGAATACATAAAGTCTCACAGCTAGTGGTAGCTTAATCCTGCCAGAGTCAGGC	480
Db	456	CTAATAAATGAATACATAAAGTCTCACAGCTAGTGGTAGCTTAATCCTGCCAGAGTCAGGC	515
Qy	481	CTCTACCTCTGTCGATGACAAATGGCACACTATGCTTTTAACTGATGTGAGCACACAAA	540
Db	516	CTCTACCTCTGTCGATGACAAATGGCACACTATGCTTTTAACTGATGTGAGCACACAAA	575

Db 1656 CAAGGGTACCTTAGAGGTCACTTCTCGGAGGCTTTCTCAACACACCTCCCGCCCTG 1715
Qy 1681 CTGCTGCTGCTCAGGCTCTCTCTCACAGCACTGATAACAGCTGTCTGCTCTCCACCT 1740
Db 1716 CTGCTGCTGCTCAGGCTCTCTCTCACAGCACTGATAACAGCTGTCTGCTCTCCACCT 1775
Qy 1741 CCCACCACTCCACTCCCAACCCAGGAAGTGAGGCGCAGAGGCGCAGAGCTGTCTGC 1800
Db 1776 CCCACCACTCCACTCCCAACCCAGGAAGTGAGGCGCAGAGGCGCAGAGCTGTCTGC 1835
Qy 1801 TGTCTCTGTGTGCGCAGGCGCCAGCAAGGGAATCTAGGAGGCTGGAGGTGCAAGGCA 1860
Db 1836 TGTCTCTGTGTGCGCAGGCGCCAGCAAGGGAATCTAGGAGGCTGGAGGTGCAAGGCA 1895
Qy 1861 GCTGGGATPAGGGTGTAGGGCTGGGTGTGAGGCTGGATCT 1903
Db 1896 GCTGGGATPAGGGTGTAGGGCTGGGTGTGAGGCTGGATCT 1938

RESULT 4
US-10-027-632-98169
; Sequence 98169, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98169
; LENGTH: 1938
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-98169

Query Match 95.1%; Score 1902.2; DB 15; Length 1938;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1901; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCTCAAGTCCATGGGTGCTGTGGTAGGAGCAGGGGATGAATGTGAACCCCTGCAATGC 60
Db 36 TCTCAAGTCCATGGGTGCTGTGGTAGGAGCAGGGGATGAATGTGAACCCCTGCAATGC 95
Qy 61 TATAGCCACCTGCTCTCTCCCTGCCCTGCATCACTACCTGGCCCTATTTTTGCTCTAG 120
Db 96 TATAGCCACCTGCTCTCTCCCTGCCCTGCATCACTACCTGGCCCTATTTTTGCTCTAG 155
Qy 121 AAGCACTGCTTCTCTATGCTCTTAGGACCACTGCGCCGATATGACAGATGAACATCGA 180
Db 156 AAGCACTGCTTCTCTATGCTCTTAGGACCACTGCGCCGATATGACAGATGAACATCGA 215
Qy 181 GGCTAAGGCAACGCAAAATCTTTCTTAAAGTCATACAGCTGTCAAAAGAAAGCTGGACA 240
Db 216 GGCTAAGGCAACGCAAAATCTTTCTTAAAGTCATACAGCTGTCAAAAGAAAGCTGGACA 275

Qy 241 ACCTGGGCAACATAGCAGATATAAAATTTTAAATTTAGCCAGATGTTAGCCCCCTG 300
Db 276 ACCTGGGCAACATAGCAGATATAAAATTTTAAATTTAGCCAGATGTTAGCCCCCTG 335
Qy 301 TAGTCTCAGGACTCAGGAGGCTGAGCAGAGGCTCACAGAGTGCAGAGTTCAAGGAT 360
Db 336 TAGTCTCAGGACTCAGGAGGCTGAGCAGAGGCTCACAGAGTGCAGAGTTCAAGGAT 395
Qy 361 GCAGTGAAGTATGATCTGCTGCACTGCACTGAAAGCTGGGTGACAGACAGACCTGGCT 420
Db 396 GCAGTGAAGTATGATCTGCTGCACTGCACTGAAAGCTGGGTGACAGACAGACCTGGCT 455
Qy 421 CTATAAATGAATACATAAAAGTCTCACAGTGTAGTGTAGTAAATCTGCGCAGAGTCAAGC 480
Db 456 CTATAAATGAATACATAAAAGTCTCACAGTGTAGTGTAGTAAATCTGCGCAGAGTCAAGC 515
Qy 481 CTCTACCTGTCTGATGACAAATGGCACATATGCTCTTTAACTGTATGACAGACCAAA 540
Db 516 CTCTACCTGTCTGATGACAAATGGCACATATGCTCTTTAACTGTATGACAGACCAAA 575
Qy 541 TGTCTTGTGAATATTTTCCCGCAGGAAAAAAGCGAAGTAGTCTTAAATCTATATATCC 600
Db 576 TGTCTTGTGAATATTTTCCCGCAGGAAAAAAGCGAAGTAGTCTTAAATCTATATATCC 635
Qy 601 ATTATATAGTCTTACCTGTGATTTGGGAAAAAAGCGAAGTCTGATTCATTTCAAGGCGG 660
Db 636 ATTATATAGTCTTACCTGTGATTTGGGAAAAAAGCGAAGTCTGATTCATTTCAAGGCGG 695
Qy 661 ACAGCCTTTGGTCACTGCTGCGGGAATTTTCAATTTTAACTCTCTAGAGGCGCT 720
Db 696 ACAGCCTTTGGTCACTGCTGCGGGAATTTTCAATTTTAACTCTCTAGAGGCGCT 755
Qy 721 TCTCATGTAAAGTCTCTGATGCGCGCAGGAGCGCGAGAGGAGGAGGAGGAGGAGGAGG 780
Db 756 TCTCATGTAAAGTCTCTGATGCGCGCAGGAGCGCGCGAGGAGGAGGAGGAGGAGGAGG 815
Qy 781 CGCCCGCAGAGGCTACGTGCGCTCTGAGCAGAGTCTCTGCTCTCTGCGCGCGCC 840
Db 816 CGCCCGCAGAGGCTACGTGCGCTCTGAGCAGAGTCTCTGCTCTCTGCGCGCGCC 875
Qy 841 AGCCCACTCCCAACACCCCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 876 AGCCCACTCCCAACACCCCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 935
Qy 901 CTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
Db 936 CTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 995
Qy 961 GCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Db 996 GCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1055
Qy 1021 TCTTCCCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db 1056 TCTTCCCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1115
Qy 1081 CTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
Db 1116 CTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1175
Qy 1141 TGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1176 TGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1235
Qy 1201 GCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Db 1236 GCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1295
Qy 1261 CGGTGGCTCTCTGCGGCTGAGGCTCTCTGCGCTGAGAGGATTAACCTGACGCGCCACGGGC 1320
Db 1296 CGGTGGCTCTCTGCGGCTGAGGCTCTCTGCGCTGAGAGGATTAACCTGACGCGCCACGGGC 1355
Qy 1321 TATGCACTGGGCTGGGCGCTTGTGGGATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380

1356 TATGACTGGCTGGGCGCTTGTGGGCATCTCCCTGCTCTCTAGGGGTTCCAGCAT 1415
1381 CGCCCCCTTTCTGAGACTCGGAAACACGCTCAGCTCCAGGACTTGTGTGCTCCTCAGTG 1440
1416 CGCCCCCTTTCTGAGACTCGGAAACACGCTCAGCTCCAGGACTTGTGTGCTCCTCAGTG 1475
1441 CACTGGGAAAGTGGGCGGCGCAGCTTTTCAGAGGGCCCTGGGAACTTCGAGAGCCAG 1500
1476 CACTGGGAAAGTGGGCGGCGCAGCTTTTCAGAGGGCCCTGGGAACTTCGAGAGCCAG 1535
1501 GTACCCCTCTCACTGTGCTCTTAGTTATCTTGATGCTCTGCTCTGCTCTGCTCTGCTCTG 1560
1536 GTACCCCTCTCACTGTGCTCTTAGTTATCTTGATGCTCTGCTCTGCTCTGCTCTGCTCTG 1595
1561 CTCCTCTCACAGGAACCTCCATCCCACTCTTGTCTGCTTGTGCTTGTGCTTGTGCTTGTG 1620
1596 CTCCTCTCACAGGAACCTCCATCCCACTCTTGTCTGCTTGTGCTTGTGCTTGTGCTTGTG 1655
1621 CAAGGGTCAGCTTAGAGGTCACTTCTTCGGAAGCTTTCCTCAACCCCTCCCGCCCTG 1680
1656 CAAGGGTCAGCTTAGAGGTCACTTCTTCGGAAGCTTTCCTCAACCCCTCCCGCCCTG 1715
1681 CTGCTGTGCTCCTCAGGCGCTCTCTCACAGCACTGATACAGCTGTGCTGTCTCCACCCCT 1740
1716 CTGCTGTGCTCCTCAGGCGCTCTCTCACAGCACTGATACAGCTGTGCTGTCTCCACCCCT 1775
1741 CCCACCACTCTCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCA 1800
1776 CCCACCACTCTCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCA 1835
1801 TGTTCTCTGTGTGTCAGGCGCCAGCAAGGAATGTAGGAGGCTGGAGGCTGCAGGGCA 1860
1836 TGTTCTCTGTGTGTCAGGCGCCAGCAAGGAATGTAGGAGGCTGGAGGCTGCAGGGCA 1895
1861 GCTGGGATAGGGCTTGAAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1903
1896 GCTGGGATAGGGCTTGAAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1938

RESULT 5
US-10-027-632-98170
; Sequence 98170, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98170
; LENGTH: 1938
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-98170

Query Match 95.1%; Score 1902.2; DB 15; Length 1938;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1901; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTCAAGTCATCGGTCCTGTAGGAGACAGGGGATCAATGTGAAACCCCTGCATGGC 60
Db 36 TCTCAAGTCATCGGTCCTGTAGGAGACAGGGGATCAATGTGAAACCCCTGCATGGC 95
QY 61 TATAGCCACCTGCTCTCCCTGCTGATCACTACCTGGCTATTTTTCGCTCTAG 120
Db 96 TATAGCCACCTGCTCTCCCTGCTGATCACTACCTGGCTATTTTTCGCTCTAG 155
QY 121 AAGCACTGCTTCTCTATGCTCTTAGGACCACTGCGCCGATATGACAGATAAGAAATCGA 180
Db 156 AAGCACTGCTTCTCTATGCTCTTAGGACCACTGCGCCGATATGACAGATAAGAAATCGA 215
QY 181 GGTAAGCAACGCAAAATCTTTTCTTAAGTCAATACAGCTGTCAAAAGAAAGCTGGACA 240
Db 216 GGTAAGCAACGCAAAATCTTTTCTTAAGTCAATACAGCTGTCAAAAGAAAGCTGGACA 275
QY 241 ACCTGGGCAACATAGCAGATATAAAATTTTAAATTTAGCCAGATGTGTAGCCCTG 300
Db 276 ACCTGGGCAACATAGCAGATATAAAATTTTAAATTTAGCCAGATGTGTAGCCCTG 335
QY 301 TAGTCTCAGGACCTCAGGAGCTCAGGAGGCTCAGAGTGCAGAGTGCAGAGTGCAGAGAT 360
Db 336 TAGTCTCAGGACCTCAGGAGGCTCAGGAGGCTCAGGAGTGCAGAGTGCAGAGTGCAGAGAT 395
QY 361 GCAGTGAAGTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 396 GCAGTGAAGTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 455
QY 421 CTAAATAATGAATACATAAAGTCTCAGAGTGTGTAGTGTAACTCTTAAATTTTAAATTTT 480
Db 456 CTAAATAATGAATACATAAAGTCTCAGAGTGTGTAGTGTAACTCTTAAATTTTAAATTTT 515
QY 481 CTCTACCTGTCTGATGACAAATGCGACACTATGCTTTTAACTGATTTGACAGACCAAA 540
Db 516 CTCTACCTGTCTGATGACAAATGCGACACTATGCTTTTAACTGATTTGACAGACCAAA 575
QY 541 TGTTTTGTGAATATTTTCCCGAGGAAACCCGAGAGTGTCTTAAATTTTAAATTTTAAATTTT 600
Db 576 TGTTTTGTGAATATTTTCCCGAGGAAACCCGAGAGTGTCTTAAATTTTAAATTTTAAATTTT 635
QY 601 ATTATATAGTTTACCTGTGATTTGGGAAACCCAGCTCTGATTTGATTTTTCAGGCGGG 660
Db 636 ATTATATAGTTTACCTGTGATTTGGGAAACCCAGCTCTGATTTGATTTTTCAGGCGGG 695
QY 661 ACAGCCTTTGGTCACTGCTGCGGGGATTTTCAATTTTAACTCTTCTTAAAGAGCGCT 720
Db 696 ACAGCCTTTGGTCACTGCTGCGGGGATTTTCAATTTTAACTCTTCTTAAAGAGCGCT 755
QY 721 TCTCATGTGTAAAGTTCTCTGATGCCCGAGGAGCCGAGAGAGGAGAGGAGGAGGAGGAGG 780
Db 756 TCTCATGTGTAAAGTTCTCTGATGCCCGAGGAGCCGAGAGAGGAGAGGAGGAGGAGGAGG 815
QY 781 CGCCCGGAGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 816 CGCCCGGAGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875
QY 841 AGCCCACTCTCCCAACACCCCTGCGGGAGAGAGCCCAAGGGGAGAGAGAGGAGGAGGAGG 900
Db 876 AGCCCACTCTCCCAACACCCCTGCGGGAGAGAGCCCAAGGGGAGAGAGAGGAGGAGGAGG 935
QY 901 CTGCCCCGAGACCTTCCGTCTCTAGTTCGAGTCTGATCGGCTTCGGACCTTCGGACCTTCG 960
Db 936 CTGCCCCGAGACCTTCCGTCTCTAGTTCGAGTCTGATCGGCTTCGGACCTTCGGACCTTCG 995
QY 961 GCTTTCGGGACCCCTGCAAGAGCTCCACAGGCGCGCTCGCTCTCTCTCTCTCTCTCTCT 1020
Db 996 GCTTTCGGGACCCCTGCAAGAGCTCCACAGGCGCGCTCGCTCTCTCTCTCTCTCTCTCT 1055
QY 1021 TCCTCCCCAGACCTCTGCGAGGAAACCGCTCATGCTAGCCCTTCGACGCTTCAGACCTCAG 1080

Db 1056 TCTTCCAGAGCCTTGGCAGAAACCGCTCACTGGTACGCCCTTCGAGCCTCAGACC 1115
QY 1081 CTGAGCGGAGACCGCTTGGCCCTCACTTAGAGCGGACCGCCGGGATGTGGCGAGTC 1140
Db 1116 CTGAGCGGAGACCGCTTGGCCCTCACTTAGAGCGGACCGCCGGGATGTGGCGAGTC 1175
QY 1141 TCGCGCTGCGCTGACCAATCGAGTGTGGGTCTCACTGAGTGGCGTCTGCCAGGCAATTA 1200
Db 1176 TCGCGCTGCGCTGACCAATCGAGTGTGGGTCTCACTGAGTGGCGTCTGCCAGGCAATTA 1235
QY 1201 GCGAGCGCTTCCCGCGCGCGCTGCCCGGCAACCCAGTGTGAGGTTGCCGTAGAAA 1260
Db 1236 GCGAGCGCTTCCCGCGCGCGCTGCCCGGCAACCCAGTGTGAGGTTGCCGTAGAAA 1295
QY 1261 CGGTGGCTCTCTGGCTGAGGCTCTCGCTGAGAGGATAAATGACGCGGCAAGGCG 1320
Db 1296 CGGTGGCTCTCTGGCTGAGGCTCTCGCTGAGAGGATAAATGACGCGGCAAGGCG 1355
QY 1321 TATGACACTGGGCTGGCGCTTGGGATCTCTCGCTGATCTCTCTAGGGGTTCCAGCAT 1380
Db 1356 TATGACACTGGGCTGGCGCTTGGGATCTCTCGCTGATCTCTCTAGGGGTTCCAGCAT 1415
QY 1381 GCGCCCTTCTGCTGGAATGGGAAACACGCTGATCCAGGACTTGTCTCTCACTG 1440
Db 1416 GCGCCCTTCTGCTGGAATGGGAAACACGCTGATCCAGGACTTGTCTCTCACTG 1475
QY 1441 CACTGGGAGAGTGGCGGGCGAGCTTTTCAGAGGGCTCGGGAATCTCCAGAGCGAG 1500
Db 1476 CACTGGGAGAGTGGCGGGCGAGCTTTTCAGAGGGCTCGGGAATCTCCAGAGCGAG 1535
QY 1501 GTCACTCTCTCACTGTGCTCTTAGTATCTTGCATGCTCTGCTCTTTGCATACGCTG 1560
Db 1536 GTCACTCTCTCACTGTGCTCTTAGTATCTTGCATGCTCTGCTCTTTGCATACGCTG 1595
QY 1561 CTCCTGACACAGAACTCTCATGCCATCTTGTCTGCTTGTGGAATCTCAGAAATCTG 1620
Db 1596 CTCCTGACACAGAACTCTCATGCCATCTTGTCTGCTTGTGGAATCTCAGAAATCTG 1655
QY 1621 CAAGGTCAGTGTAGAGTCACTTCTCCGGAAGCTTCTCAACACCTCCCGCCCTG 1680
Db 1656 CAAGGTCAGTGTAGAGTCACTTCTCCGGAAGCTTCTCAACACCTCCCGCCCTG 1715
QY 1681 CTGCTGTGCTCTCAGGCTCTCTCAACAGCTGATGAGTGTGCTCTCCAGCTTCCACCT 1740
Db 1716 CTGCTGTGCTCTCAGGCTCTCTCAACAGCTGATGAGTGTGCTCTCCAGCTTCCACCT 1775
QY 1741 CCCACCTCTCACTCCACCCAGGAGTGAAGCCAGAGGCGGACGAGTGTGCTG 1800
Db 1776 CCCACCTCTCACTCCACCCAGGAGTGAAGCCAGAGGCGGACGAGTGTGCTG 1835
QY 1801 TGTCTCTGTGTGCCAGGCGCCAGCAAGGGAATGTAGGAGGTTGGAGGTGCGAGGCA 1860
Db 1836 TGTCTCTGTGTGCCAGGCGCCAGCAAGGGAATGTAGGAGGTTGGAGGTGCGAGGCA 1895
QY 1861 GCTGGGATTAGGCTTGGGCTGGGTGTTGGAGGCTGGATCT 1903
Db 1896 GCTGGGATTAGGCTTGGGCTGGGTGTTGGAGGCTGGATCT 1938

RESULT 6

US-10-027-632-41182
; Sequence 41182, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41182
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-41182

Query Match 29.9%; Score 597.6; DB 13; Length 598;
Best Local Similarity 99.8%; Pred. No. 1.2e-173;
Matches 597; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 116 TCTAGAGCACTGCTTCTCTATGCTCTTAGGACCACTGCGCGATATGACAGTAAGAAC 175
Db 1 TCTAGAGCACTGCTTCTCTATGCTCTTAGGACCACTGCGCGATATGACAGTAAGAAC 60
QY 176 ATCGAGGCTAAGCAACGCAAAATCTTTCTTAAAGTCTACAGCTGTCAAAAGAAAGCT 235
Db 61 ATCGAGGCTAAGCAACGCAAAATCTTTCTTAAAGTCTACAGCTGTCAAAAGAAAGCT 120
QY 236 GGACAACTGGGCAACATAGCGAGATAAAAAATTTAAATAGCCAGATGTGGTAGCC 295
Db 121 GGACAACTGGGCAACATAGCGAGATAAAAAATTTAAATAGCCAGATGTGGTAGCC 180
QY 296 CCCTGTAGTCTCAGCGACTCAGGAGGCTCAGGAGGCTCAGGAGGCTCAGGAGGCTCA 355
Db 181 CCCTGTAGTCTCAGCGACTCAGGAGGCTCAGGAGGCTCAGGAGGCTCAGGAGGCTCA 240
QY 356 AGATGCACTGAGTATGATCTGCACTGCACTGAAAGCTGGGTGACAGCAAGAGCC 415
Db 241 AGATGCACTGAGTATGATCTGCACTGCACTGAAAGCTGGGTGACAGCAAGAGCC 300
QY 416 TGCTCTAATAATGAATACATAAAGTCTCAGCTAGTGGTAGCTAATCTCTGCCAGCT 475
Db 301 TGCTCTAATAATGAATACATAAAGTCTCAGCTAGTGGTAGCTAATCTCTGCCAGCT 360
QY 476 CAGGCTCTACCTGTCTGATGACAAATGGCACTATGTCTTTAACTGATTGAGAGCC 535
Db 361 CAGGCTCTACCTGTCTGATGACAAATGGCACTATGTCTTTAACTGATTGAGAGCC 420
QY 536 ACAATGTTTCTGTAATATTTTCCCGAGGAAAAACCGGAAGTAGTCTTAATTTCTATA 595
Db 421 ACAATGTTTCTGTAATATTTTCCCGAGGAAAAACCGGAAGTAGTCTTAATTTCTATA 480
QY 596 CATCCATTATATTAGTATTTTACCTGTGGATTGGGAAAAACCCAGCTCTGATTTCAGG 655
Db 481 CATCCATTATATTAGTATTTTACCTGTGGATTGGGAAAAACCCAGCTCTGATTTCAGG 540
QY 656 GCGGACAGCCCTTGGTGCACCTGTCTGCGGGAATTTCCATTTAACTCTCTCTAGA 713
Db 541 GCGGACAGCCCTTGGTGCACCTGTCTGCGGGAATTTCCATTTAACTCTCTCTAGA 598

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US-10-027-632-41182
; Sequence 41182, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME

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; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41182
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-41182

Query Match      29.9%; Score 597.6; DB 15; Length 598;
Best Local Similarity 99.8%; Pred. No. 1.2e-173;
Matches 597; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 116 TCTAGAGCACTGCTTCTATGCTTCCTTAGGACCACTGCCGATATGACAGATAGAAC 175
Db      |||
QY 176 ATCAGAGCTAAGGCAACGCAAACTTTTCTTAAAGTCATACAGCTCTCAAAAGAGCT 235
Db      |||
QY 61 ATCAGAGCTAAGGCAACGCAAACTTTTCTTAAAGTCATACAGCTCTCAAAAGAGCT 120
QY 236 GGACAACTGGGCAACATAGCGATATAAAATTTTAAATTAATGACAGATGGTAGCC 295
Db      |||
QY 121 GGACAACTGGGCAACATAGCGATATAAAATTTTAAATTAATGACAGATGGTAGCC 180
QY 296 CCCTGTAGTCTCAGCGACTCAGGAGGCTGAGGAGGAGGCTCAGGAGTGCAGAGTTCA 355
Db      |||
QY 181 CCCTGTAGTCTCAGCGACTCAGGAGGCTGAGGAGGAGGCTCAGGAGTGCAGAGTTCA 240
QY 356 AGGATGAGTGAAGTATGATCTGCCACTGCCTGAAAGCTGGGTGACAGCAAGACCC 415
Db      |||
QY 241 AGGATGAGTGAAGTATGATCTGCCACTGCCTGAAAGCTGGGTGACAGCAAGACCC 300
QY 416 TGGCTCTAATAAATCAATACATAAAGTCTCACAGTCTAGTGGTAGCTTAATCTGCGAGAGT 475
Db      |||
QY 301 TGGCTCTAATAAATCAATACATAAAGTCTCACAGTCTAGTGGTAGCTTAATCTGCGAGAGT 360
QY 476 CAGGCTCTACCTGCTGTGATGACAAATGGCACTATGCTTTTAACTGATTCAGACCC 535
Db      |||
QY 361 CAGGCTCTACCTGCTGTGATGACAAATGGCACTATGCTTTTAACTGATTCAGACCC 420
QY 536 ACAATGTTTTGTGAATTTTCCCGAGGAAAAACCGGAAGTAGTCTTAAATTTCTATA 595
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QY 421 ACAATGTTTTGTGAATTTTCCCGAGGAAAAACCGGAAGTAGTCTTAAATTTCTATA 480
QY 596 CATCCATTATATTAGTTTTTACCTGTGGATTGGGAAAAACCCAGCTCTGATTCATTTCAGG 655
Db      |||
QY 481 CATCCATTATATTAGTTTTTACCTGTGGATTGGGAAAAACCCAGCTCTGATTCATTTCAGG 540
QY 656 GCGGAGACGCTTTGGTGCATGCTGCGGAGATTTTCCATTTTAACTCTCTCTAGA 713
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QY 541 GCGGAGACGCTTTGGTGCATGCTGCGGAGATTTTCCATTTTAACTCTCTCTAGA 598

RESULT 8
US-09-864-761-9542/c
; Sequence 9542, Application US/09864761

; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9542
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002472.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 18
US-09-864-761-9542

Query Match      28.1%; Score 563; DB 9; Length 563;
Best Local Similarity 100.0%; Pred. No. 5.6e-163;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 CACTGAAGCTGGGTGACAGAGCAAGCCCTGGCTCTAATAATGAATACATATAAGTCTC 445
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QY 563 CACTGAAGCTGGGTGACAGAGCAAGCCCTGGCTCTAATAATGAATACATATAAGTCTC 504
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QY 446 ACAGCTAGTGTAGTAAATCCTGCCAGAGTCAGGCTCTACCTGTCTGTGATGACAAATGGC 505
Db 503 ACAGCTAGTGTAGTAAATCCTGCCAGAGTCAGGCTCTACCTGTCTGTGATGACAAATGGC 444
QY 506 ACACATATGCTCTTTAACTGATTCAGACCAACAAATGTTTCTGAATATTTTCCCCAGGG 565
Db 443 ACACATATGCTCTTTAACTGATTCAGACCAACAAATGTTTCTGAATATTTTCCCCAGGG 384
QY 566 AAAAAACCGAAGTAGTCTTAAATCTATACATCCATATATAGTTTAACTGTGGATT 625
Db 383 AAAAAACCGAAGTAGTCTTAAATCTATACATCCATATATAGTTTAACTGTGGATT 324
QY 626 GGGAAAAACCCAGCTCTGATTCATTCAGGGGGGAGACGCTTTGGTGCATCTGCTGGCG 685
Db 323 GGGAAAAACCCAGCTCTGATTCATTCAGGGGGGAGACGCTTTGGTGCATCTGCTGGCG 264
QY 686 GGAATTTTCATTTAACTCTCTCTAGAGCGCTTCTCATGGTAAAGTTCTCTGATGCGG 745
Db 263 GGAATTTTCATTTAACTCTCTCTAGAGCGCTTCTCATGGTAAAGTTCTCTGATGCGG 204
QY 746 CCAGGAGCGCCGAGGAGGGGAGGCGCTGGAGAGCGCCGCGAGGGCTACGTGCCCT 805
Db 203 CCAGGAGCGCCGAGGAGGGGAGGCGCTGGAGAGCGCCGCGAGGGCTACGTGCCCT 144
QY 806 GCTGACACAGAGTCTCTCTGCTCTCTGCGGGCGCCAGCCACCTCCCAACACCCCTGCGG 865
Db 143 GCTGACACAGAGTCTCTCTGCTCTCTGCGGGCGCCAGCCACCTCCCAACACCCCTGCGG 84
QY 866 GAGAGCGCCGAGGAGGAGAGCGGCTGCGCCCTGCGCCGCGAGACCTTCCGTCTCTA 925
Db 83 GAGAGCGCCGAGGAGGAGAGCGGCTGCGCCCTGCGCCGCGAGACCTTCCGTCTCTA 24
QY 926 GGTGGAGTCTGAATCGGCGCTTG 948
Db 23 GGTGGAGTCTGAATCGGCGCTTG 1

RESULT 9

US-09-864-761-9446/c
; Sequence 9446, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9446
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002472.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
US-09-864-761-9446

Query Match 27.7%; Score 554; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 3.4e-160;
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 ACCTGTGGATTGGAAAAACCCAGCTCTGATTCGATTTTCAGGGCGGACAGCCTTTGGTGC 674
Db 554 ACCTGTGGATTGGAAAAACCCAGCTCTGATTCGATTTTCAGGGCGGACAGCCTTTGGTGC 495
QY 675 ACTGTCTGGCGGATTTTCCATTTTAACTCTCTTAGAAGCGCCTTCTCATGTTAAAGT 734
Db 494 ACTGTCTGGCGGATTTTCCATTTTAACTCTCTTAGAAGCGCCTTCTCATGTTAAAGT 435
QY 735 TCTGTATGCCCGCAGGAGCGCCGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 794
Db 434 TCTGTATGCCCGCAGGAGCGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 375
QY 795 CTACGTGCCCTGTCTGGACAGAGGTCTCTGCTCTCTCTGCGCGCGCGCGCGCGCGCGCGCG 854
Db 374 CTACGTGCCCTGTCTGGACAGAGGTCTCTGCTCTCTCTGCGCGCGCGCGCGCGCGCGCGCG 315
QY 855 AACCCCTGCGGAGAGAGCCGCCAAGGGAGGAGAGCGGGCTGCGCCCTGCGCCCGAGCACC 914
Db 314 AACCCCTGCGGAGAGAGCCGCCAAGGGAGGAGAGCGGGCTGCGCCCTGCGCCCGAGCACC 255
QY 915 TTCGGTCTCTAGGTGGAGTCTGAATCGGCCCTTGGGAGCCCTGCTTGGCTTCGGGGACCCC 974
Db 254 TTCGGTCTCTAGGTGGAGTCTGAATCGGCCCTTGGGAGCCCTGCTTGGCTTCGGGGACCCC 195
QY 975 TGCAAGACGTCACAGGCGCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1034
Db 194 TGCAAGACGTCACAGGCGCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
QY 1035 CTGGCAGGAGACCGCTCATCTGTTACGCCCTTTTCGAGAGCTTCAGAGGAGGAGGAGGAGG 1094
Db 134 CTGGCAGGAGACCGCTCATCTGTTACGCCCTTTTCGAGAGCTTCAGAGGAGGAGGAGGAGG 75
QY 1095 GCTTGGCGCTCTACATTTAGAGCGCGAGCCCGGGGATGTGGGCGGAGTCTGGGCTGGCTGA 1154
Db 74 GCTTGGCGCTCTACATTTAGAGCGCGAGCCCGGGGATGTGGGCGGAGTCTGGGCTGGCTGA 15
QY 1155 CCAATCGAGTGGG 1168
Db 14 CCAATCGAGTGGG 1

RESULT 10

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Job time : 991.76 secs

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; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 51289
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-648

Query Match 5.4%; Score 108.2; DB 17; Length 51289;
Best Local Similarity 75.1%; Pred. No. 1.7e-21;
Matches 148; Conservative 0; Mismatches 48; Indels 1; Gaps 1;
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DB 18038 GCAAGACCCCGTCTTACAAAAATAAAATTTAGCCAGGTGTCCACACACCTGTAGTCC 18097
QY 307 CAGCGACTCAGGAGGCTGAGCGAGGAGGCTCACCAGAGTGCA-GAGTTCAAGGATGCAGT 365
DB 18098 CAGCTACTCGGGAGGCTGAGCGAGGAGATCACTTGAGCCCGAGGAGTTCAAGGTTGCAGT 18157
QY 366 GAGCTATGATCCTCCCACTGCACCTGAAAGCTGGGTGACAGCAAGACCCCTGGCTCTAAT 425
DB 18158 GCACITTTGATCATGCCACTGCACCTCCAGCCTGGGTGAAAAAGCAGACCCCTATCTCTAAA 18217
QY 426 AAATGAATACATAAAGT 442
DB 18218 GAATGCATAATAAATT 18234

RESULT 15
US-09-799-799-3
; Sequence 3, Application US/09799799
; Patent No. US20020132291A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C0001157
; CURRENT APPLICATION NUMBER: US/09/799,799
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 88191
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(88191)
; OTHER INFORMATION: n = A,T,C or G
US-09-799-799-3

Query Match 5.2%; Score 103.2; DB 9; Length 88191;
Best Local Similarity 69.8%; Pred. No. 7.8e-20;
Matches 155; Conservative 0; Mismatches 63; Indels 4; Gaps 1;
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DB 2226 TCAAGACCAAGCTGGGCAACATTGTGAATCTCTGCAAAAAATACACAAATAAGCC 2285
QY 283 AGAT---GTGGTAGCCCTCTAGTCTCAGCGACTCAGGAGGCTGAGCGAGGAGGCTCA 338
DB 2286 AGTTGTGTGGCTGCGCTGTAGTCCAGCTACTCGGAGACTGAGTGGGAGGATTG 2345
QY 339 CCAGAGTCAGAGTTCAAGGATGAGTGAGTATGATCTCCCACTGCACCTGAAGCTGG 398
DB 2346 CTTGAACCCAGAGGTTGAGGCTGAGTGAGTGTGATTTGCCACTGCACCTAGCCTGG 2405
QY 399 GTGACAGAGCAAGCCCTGGCTCTAAATAAATGAATACATAAA 440
DB 2406 GTGACAGAGCGAGACCCCTGTCTCAAAAAAATTAATTAATAA 2447

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SUMMARIES

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5	95	4.8	59065	4	US-10-135-696-3
6	92	4.6	1381	2	US-08-454-557C-49
7	92	4.6	1381	2	US-08-340-426D-49
8	92	4.6	1381	2	US-08-450-673C-49
9	92	4.6	1381	5	PCT-US95-1711A-49
10	90.6	4.5	1001	4	US-09-641-638-78
11	90.6	4.5	1001	4	US-10-170-097-78
12	90.6	4.5	35060	3	US-08-814-095-7
13	89.8	4.5	66804	4	US-09-740-041-3
14	89.4	4.5	83450	4	US-09-811-469-3
15	89.4	4.5	83450	4	US-10-370-659-3
16	89	4.5	7676	1	US-08-451-777A-7
17	89	4.5	7676	2	US-08-451-778A-7
18	89	4.5	7676	2	US-08-998-208-7
19	89	4.5	7676	5	PCT-US95-06743-7
20	89	4.5	8133	3	US-09-659-791A-10
21	88.4	4.4	435	4	US-09-621-976-16669
22	88.4	4.4	472	4	US-09-621-976-16669
23	88.4	4.4	13674	2	US-08-852-807-10
24	88.4	4.4	13674	2	US-08-852-807-1
25	88.2	4.4	31000	4	US-09-966-451-10
26	88.2	4.4	64467	4	US-09-803-671B-3
27	88	4.4	18443	3	US-09-078-294-6
28	88	4.4	18443	3	US-09-078-294-6

C	28	88	4.4	114793	4	US-10-148-806-3	Sequence 3, Appli
C	29	87.8	4.4	8453	3	US-09-167-681-45	Sequence 45, Appli
C	30	87.4	4.4	51719	4	US-09-918-686-2	Sequence 2, Appli
C	31	87.4	4.4	92139	4	US-09-918-686-2	Sequence 1, Appli
C	32	87.4	4.4	98844	4	US-09-791-211-10	Sequence 10, Appli
C	33	86.8	4.3	5310	4	US-09-620-312D-623	Sequence 623, Appli
C	34	86.8	4.3	66933	4	US-09-544-398B-11	Sequence 11, Appli
C	35	86.8	4.3	66933	4	US-09-543-771-11	Sequence 11, Appli
C	36	86.8	4.3	72049	4	US-09-544-398B-9	Sequence 9, Appli
C	37	86.8	4.3	72049	4	US-09-543-771-9	Sequence 9, Appli
C	38	86.8	4.3	81001	4	US-09-750-580-1	Sequence 1, Appli
C	39	86.6	4.3	15849	4	US-09-054-272-50	Sequence 50, Appli
C	40	86.6	4.3	36551	3	US-09-738-894A-3	Sequence 3, Appli
C	41	86.6	4.3	36651	4	US-09-964-469-3	Sequence 3, Appli
C	42	86.4	4.3	6235	3	US-09-305-384-5	Sequence 5, Appli
C	43	86.4	4.3	6235	4	US-09-525-160B-6	Sequence 6, Appli
C	44	86.4	4.3	6679	3	US-09-305-384-1	Sequence 1, Appli
C	45	86.4	4.3	6679	4	US-09-525-160B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-191-136-27
; Sequence 27, Application US/09191136B
; Patent No. 6214581
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding A Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
; TITLE OF INVENTION: And Use Thereof
; FILE REFERENCE: 6293 US.P1
; CURRENT APPLICATION NUMBER: US/09/191,136B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 09/008,526
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 09/008,185
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,298
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,669
; EARLIER FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Universal Amplification Sequencing Primer
US-09-191-136-27

Query Match 8.0%; Score 159; DB 3; Length 394;
Best Local Similarity 91.8%; Pred No. 54e-33;
Matches 168; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	1818	GGCCACGAGAAAGGAAATGTAGGAGGGTGGAGGTCAGGCGAGCTGGGATTAGGGGTTG	1877
DB	1	GGCCACGAGTCTACGTAGTACGGGGGGGGGGTGCAGGCGAGCTGGGATTAGGGGTTG	60
QY	1878	AGGGTGGGTGTGGAGGCTGGATCTGATCTCTGTTAGTGGAGTGTCCCTTTAAACAG	1937
DB	61	AGGGTGGGTGTGGAGGCTGGATCTGATCTCTGTTAGTGGAGTGTCCCTTTAAACAG	120
QY	1938	CAACTGGGCTGCGCTGGCTGGCGCCCTGCTTTGCTCTGTTACGTCGGGTGAGCTG	1997
DB	121	CAACTGGGCTGCGCTGGCTGGCGCCCTGCTTTGCTCTGTTACGTCGGGTGAGCTG	180
QY	1998	CCA 2000	

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Db      181 CCA 183
|||||
30025 AGGCATGGTGGTGCACCTGTAGTCCAGCTACTCAGGAGGCTGAGCGAGGAGTCTC 30084
QY      340 CAGAGTGCAGAGTTCAAGGATGCAGTGCAGTATGATCCTGCCACTGCACCTGAAAGCTGGG 399
Db      30085 TTGAGCCTGGGAGGTCAGACTACAGTGCAGCAATGATTTGTGCCACTGCACCTCCAGCCTGGG 30144
QY      400 TGACAGACCAAGACCCCTGGCTCTTAATAAATGAATACATAAAGTCTCACAGCTAGTGTA 458
Db      30145 TGACAGAGTAAGACTGTCTCTTTAAAAAAGTGTGATTTCTATTGGTA 30203

RESULT 4
US-09-978-197-3
; Sequence 3, Application US/09978197
; Patent No. 6403353
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178DIV
; CURRENT APPLICATION NUMBER: US/09/978,197
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/813,817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-978-197-3

Query Match      4.8%; Score 95; DB 4; Length 59065;
Best Local Similarity 65.3%; Pred. No. 8.2e-15;
Matches 156; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

QY      223 TCAAAAGAAAGCTGGCAACCTGGGCAACATAGCGAGATAAAAAATTTTAAATTAGCC 282
Db      29965 TTAAGACCAAGCTGGGCAACATAGGGAGACCCCTCTCTACAAAAATAAAAAATTAGCC 30024
QY      283 AG---ATGTGTGATCCCTCTGTACTCTCAGCGACTCAGGAGGCTGAGCGAGGAGGCTCAC 339
Db      30025 AGGCATGGTGGTGCACCTGTAGTCCAGCTACTCAGGAGGCTGAGCGAGGAGTCTC 30084
QY      340 CAGAGTGCAGAGTTCAAGGATGCAGTGCAGTATGATCCTGCCACTGCACCTGAAAGCTGGG 399
Db      30085 TTGAGCCTGGGAGGTCAGACTACAGTGCAGCAATGATTTGTGCCACTGCACCTCCAGCCTGGG 30144
QY      400 TGACAGACCAAGACCCCTGGCTCTTAATAAATGAATACATAAAGTCTCACAGCTAGTGTA 458
Db      30145 TGACAGAGTAAGACTGTCTCTTTAAAAAAGTGTGATTTCTATTGGTA 30203

RESULT 5
US-10-135-696-3
; Sequence 3, Application US/10135696
; Patent No. 6740513
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178DIV
; CURRENT APPLICATION NUMBER: US/10/135,696
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 09/813,817
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/978,197
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0

Query Match      4.8%; Score 95; DB 3; Length 59065;
Best Local Similarity 65.3%; Pred. No. 8.2e-15;
Matches 156; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

QY      223 TCAAAAGAAAGCTGGCAACCTGGGCAACATAGCGAGATAAAAAATTTTAAATTAGCC 282
Db      29965 TTAAGACCAAGCTGGGCAACATAGGGAGACCCCTCTCTACAAAAATAAAAAATTAGCC 30024
QY      283 AG---ATGTGTGATCCCTCTGTACTCTCAGCGACTCAGGAGGCTTTCGAGCCT 1074
Db      40 CTGCGAGAAACCGCTCATCGTTAGCGCCCTTTTCGAGCCT 1

RESULT 3
US-09-813-817-3
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match      4.8%; Score 95; DB 3; Length 59065;
Best Local Similarity 65.3%; Pred. No. 8.2e-15;
Matches 156; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

QY      223 TCAAAAGAAAGCTGGCAACCTGGGCAACATAGCGAGATAAAAAATTTTAAATTAGCC 282
Db      29965 TTAAGACCAAGCTGGGCAACATAGGGAGACCCCTCTCTACAAAAATAAAAAATTAGCC 30024
QY      283 AG---ATGTGTGATCCCTCTGTACTCTCAGCGACTCAGGAGGCTGAGCGAGGAGTCTC 339

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; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-135-696-3

Query Match      4.8%; Score 95; DB 4; Length 59065;
Best Local Similarity 65.3%; Pred. No. 8.2e-15;
Matches 156; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

QY 223 TCAAAAGAAAGCTGGACAACTGGGCAACATAGCGAGATAAAATAATTTAAATAGCC 282
DB 29965 TTAAGACCGCTGGGCAACATAGGGAGACCTGTCTACAAAAATAAAATTTAGCC 30024

QY 283 AG--ATGTGTAGCCCTGTAGTCTCAGCGATCTAGGAGGCTGAGCGAGAGGCTCAC 339
DB 30025 AGGCATGTGTGTGTCACCTGTAGTCCAGCTACTCAGAGGCTGAGCGAGGATCTC 30084

QY 340 CAGAGTCAGAGTTCAGGATGCAAGTATGATCTCCCATGCTGCACTGAAAGCTGG 399
DB 30085 TTGAGCCTGGGAGTCAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 30144

QY 400 TGACAGACAAAGCCCTGGCTCTAATAAATGAATACATAAAGTCTCAGCTAGTGTA 458
DB 30145 TGACAGAGTAAGACTCTGTCTCTTAAAAAATAAAAGTTGATTTCTATTGGA 30203

RESULT 6
US-08-454-557C-49/c
; Sequence 49, Application US/08454557C
; Patent No. 5830570
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-454-557C-49

Query Match      4.6%; Score 92; DB 2; Length 1381;
Best Local Similarity 69.5%; Pred. No. 9.3e-15;
Matches 139; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 261 TAAAAAATTAATTAATTAAGCAGATGTTAGCCCTGTAGTCTCAGGACTCAGGAG 320
```

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DB 785 TAAAAATACAAAAAATTAGCTAGCGGTGGGCGCTGTAGTCCAGCTACTCAGGAG 726
QY 321 GCTGAGCGCAGGAGGCTCACCAGAGTGC-AGAGTTCAAGGATGACAGTATGATCCTG 379
DB 725 GCTGGGGCAGGAGAGATAACTTGAACCCGGGAGAGAGGTTGCACTGAGCCAAAGATTGCG 666
QY 380 CCACTGCACTGAAAGCTGGGTGACAGAGCAAGACCCCTGGCTCTAATAATGAATACATAA 439
DB 665 CCACTGCACTCAGCGCTGGGTGACAGAGTGAGTCTGTCTCAAAAAATTTAAAAATAAAA 606
QY 440 AGTCTCACAGCTAGTGGTAG 459
DB 605 AAAAAAATTACCAGGTGTAG 586

RESULT 7
US-08-340-426D-49/c
; Sequence 49, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-340-426D-49

Query Match      4.6%; Score 92; DB 2; Length 1381;
Best Local Similarity 69.5%; Pred. No. 9.3e-15;
Matches 139; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 261 TAAAAAATTAATTAATTAAGCAGATGTTAGCCCTGTAGTCTCAGGACTCAGGAG 320
DB 785 TAAAAATACAAAAAATTAGCTAGCGGTGGGCGCTGTAGTCCAGCTACTCAGGAG 726
QY 321 GCTGAGCGCAGGAGGCTCACCAGAGTGC-AGAGTTCAAGGATGACAGTATGATCCTG 379
DB 725 GCTGGGGCAGGAGAGATAACTTGAACCCGGGAGGAGGTTGCACTGAGCCAAAGATTGCG 666
QY 380 CCACTGCACTGAAAGCTGGGTGACAGAGCAAGACCCCTGGCTCTAATAATGAATACATAA 439
DB 665 CCACTGCACTCCAGCGCTGGGTGACAGAGTGAGTCTGTCTCAAAAAATTTAAAAATAAAA 606
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QY 440 AGTCTCAGCTAGTGGTAG 459
 Db 605 ATAAAAATTACCAGGTGTAG 586

RESULT 8

US-08-450-673C-49/c
 ; Sequence 49, Application US/08450673C
 ; Patent No. 594888
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; APPLICANT: Wangs, Jack R.
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 ; TITLE OF INVENTION: of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,673C
 FILING DATE: 30-MAY-1995
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36,203
 REFERENCE/DOCKET NUMBER: 0609.3840004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1381 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 US-08-450-673C-49

Query Match 4.6%; Score 92; DB 2; Length 1381;
 Best Local Similarity 69.5%; Pred. No. 9.3e-15;
 Matches 139; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
 QY 261 TAAAAAATTATTTAAATAGCCAGATGTGTAGCCCTCTGTAGTCTCAGCGACTCAGGAG 320
 Db 785 TAAAAATACAAAAAATTAGTAGGCGTGTGGCGCCTGTAGTCCAGCTACTCAGGAG 726
 QY 321 GCTGAGCAGGAGGCTCACCAGAGTGC-AGAGTTCAAGGATGCGAGTGTATGATCTCTG 379
 Db 725 GCTGGGCGCAGGAGATAAATCTGAACCCGGGAGGCGAGAGGTTGCGTAGCCCAAGATTGGC 666
 QY 380 CCAGTGCACCTGAAAGCTGGGTGACAGAGCAAGACCTGCTCTAATAAATGAATACATAA 439
 Db 665 CCAGTGCACCTCCAGCCTGGGTGACAGAGTGAGACTCTGTCTCAAAAAATTAAAAATAAAA 606
 QY 440 AGTCTCAGCTAGTGGTAG 459
 Db 605 ATAAAAATTACCAGGTGTAG 586

RESULT 9

PCT-US95-17111A-49/c
 ; Sequence 49, Application PC/TUS951711A
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; APPLICANT: Wangs, Jack R.

; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
 ; TITLE OF INVENTION: Detection of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/17111A
 ; FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/340,426
 FILING DATE: 14-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36,203
 REFERENCE/DOCKET NUMBER: 0609.3840002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1381 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 PCT-US95-17111A-49

Query Match 4.6%; Score 92; DB 5; Length 1381;
 Best Local Similarity 69.5%; Pred. No. 9.3e-15;
 Matches 139; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
 QY 261 TAAAAAATTATTTAAATAGCCAGATGTGTAGCCCTCTGTAGTCTCAGCGACTCAGGAG 320
 Db 785 TAAAAATACAAAAAATTAGTAGGCGTGTGGCGCCTGTAGTCCAGCTACTCAGGAG 726
 QY 321 GCTGAGCAGGAGGCTCACCAGAGTGC-AGAGTTCAAGGATGCGAGTGTATGATCTCTG 379
 Db 725 GCTGGGCGCAGGAGATAAATCTGAACCCGGGAGGCGAGAGGTTGCGTAGCCCAAGATTGGC 666
 QY 380 CCAGTGCACCTGAAAGCTGGGTGACAGAGCAAGACCTGCTCTAATAAATGAATACATAA 439
 Db 665 CCAGTGCACCTCCAGCCTGGGTGACAGAGTGAGACTCTGTCTCAAAAAATTAAAAATAAAA 606
 QY 440 AGTCTCAGCTAGTGGTAG 459
 Db 605 ATAAAAATTACCAGGTGTAG 586

RESULT 10

US-09-641-638-78/c
 ; Sequence 78, Application US/09641638
 ; Patent No. 6432648
 ; GENERAL INFORMATION:
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Chumakov, Ilya
 ; APPLICANT: Cohen, Annick
 ; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
 ; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
 ; FILE REFERENCE: GENSET.051CPI
 ; CURRENT APPLICATION NUMBER: US/09/641,638
 ; CURRENT FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: US 09/502,330

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; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 09/502,330
; SOFTWARE: Patent.pm
; NUMBER OF SEQ ID NOS: 1304
; SEQ ID NO 78
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 10-224-341 : polymorphic base C or T
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 10-224-341.misl, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 10-224-341.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 161..179
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 561..580
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 10-224-341 potential probe
; NAME/KEY: misc_feature
; LOCATION: 732
; OTHER INFORMATION: n=a, g, c or t
; OTHER INFORMATION: n=a, g, c or t
US-09-641-638-78

Query Match          4.5%; Score 90.6; DB 4; Length 1001;
Best Local Similarity 72.2%; Pred. No. 1.9e-14;
Matches 117; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 287 GTGGTAGCCCTCTAGTCTCAGGAGCTCAGGAGGCTGAGGAGGCTCACCAGAGTG 346
Db 748 GTGGTAGCCCTCTANTCCAGTACTCAGGAGCTGAGGAGGAGTGTGTCAGCC 689

QY 347 CAGAGTTCAAGGATGAGTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 406
Db 688 CAGGAATTAGGATGCGGTGAGCCATGATTGTGCTGCTGCTGCTGCTGCTGCTG 629

QY 407 GCAAGACCTCGCTCTAATAATGATATGATATGATATGATATGATATGATATG 448
Db 628 GTGAGACCTCTCTCAAAAATACAAACAAACAAACAAACA 587

RESULT 11
US-10-170-097-78/c
; Sequence 78, Application US/10170097
; Patent No. 6794143
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
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; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 09/502,330
; SOFTWARE: Patent.pm
; NUMBER OF SEQ ID NOS: 1304
; SEQ ID NO 78
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 10-224-341 : polymorphic base C or T
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 10-224-341.misl, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 10-224-341.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 161..179
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 561..580
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 10-224-341 potential probe
; NAME/KEY: misc_feature
; LOCATION: 732
; OTHER INFORMATION: n=a, g, c or t
; OTHER INFORMATION: n=a, g, c or t
US-10-170-097-78

Query Match          4.5%; Score 90.6; DB 4; Length 1001;
Best Local Similarity 72.2%; Pred. No. 1.9e-14;
Matches 117; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 287 GTGGTAGCCCTCTAGTCTCAGGAGCTCAGGAGGCTGAGGAGGCTCACCAGAGTG 346
Db 748 GTGGTAGCCCTCTANTCCAGTACTCAGGAGCTGAGGAGGAGTGTGTCAGCC 689

QY 347 CAGAGTTCAAGGATGAGTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 406
Db 688 CAGGAATTAGGATGCGGTGAGCCATGATTGTGCTGCTGCTGCTGCTGCTGCTG 629

QY 407 GCAAGACCTCGCTCTAATAATGATATGATATGATATGATATGATATGATATG 448
Db 628 GTGAGACCTCTCTCAAAAATACAAACAAACAAACAAACA 587

RESULT 12
US-08-814-095-7
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
```

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STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO.: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHS gene"
DESCRIPTION: Promotor, ACHS gene and ARS gene"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
FEATURE:
NAME/KEY: promotor
LOCATION: 4089..22464
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[illegible]

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(83450)
; OTHER INFORMATION: n = A,T,C or G
US-10-370-659-3

Query Match          4.5%; Score 89.4; DB 4; Length 83450;
Best Local Similarity 65.9%; Pred. No. 3.1e-13;
Matches 176; Conservative 0; Mismatches 86; Indels 5; Gaps 3;

Qy 223 TCAAAAGAAAGCTGGACAACCTGG-GCAACATAGCGAGATAAAAAATTTAAATTAGC 281
Db 60641 TCAAGACCAGCCTGGCCCAACATGGTGAACCTTGTCTCTCTTAAATAACAAAAATTAGC 60700

Qy 282 CAGATGTGGTAGC---CCCCTGTAGTCTCAGCGACTCAGGAGGCTGAGCGAGGCTCA 338
Db 60701 CAGCATGGTGGCAGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGCGAGGAGATCA 60760

Qy 339 CCAGAGTGCAGAGTTCA-AGGATGCACTGAGCTATGATCCTGCCACTGCACTGAAAAGCTG 397
Db 60761 CTTCAACCTGGAGGCAGAGGTTGCATTGATCAAGATCACGCCACTGCACTGCAGCCTG 60820

Qy 398 GGTGACAGAGCAGACCCCTGGCTCTAATAAATGAATACATAAAGTCTCAGAGTAGTGGT 457
Db 60821 GGTGATAGACCAAGTCTCCATCTCAAAAAAATAATTTACAAAGTGGGCCGGTTGTGGT 60880

Qy 458 AGCTAATCTCTGCCAGAGTCAAGGCTCT 484
Db 60881 AGCTATGCCAGTAAATCCAAAGCTCT 60907
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Search completed: November 21, 2004, 17:43:07
Job time : 169.842 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 21, 2004, 12:30:45 ; Search time 958.553 Seconds
(without alignments)
10952.804 Million cell updates/sec

Title: US-09-820-095B-3_COPY_1_2000
Perfect score: 2000
Sequence: 1 tctccaagtcacatgggtgcc.....agctgcggctgcagctgccca 2000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:.*
1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2000	100.0	16449	8 AAL51049	Human P2X
2	563	28.1	563	4 AAI18897	Probe #88
3	563	28.1	563	4 ABA63896	Human foe
4	563	28.1	563	4 AAI44018	Probe #12
5	563	28.1	563	4 ABA31076	Probe #95
6	563	28.1	563	4 AAK38120	Human bon
7	563	28.1	563	4 AAK12404	Human bra
8	563	28.1	563	4 ABS37739	Human liv
9	563	28.1	563	6 ABS12139	Human gen
10	554	27.7	554	4 AAI43912	Probe #12
11	554	27.7	554	4 ABA30380	Probe #94
12	554	27.7	554	6 ABS12029	Human gen
13	458.4	22.9	1904	10 ADA53808	Human cod
14	383.2	19.2	508	12 ACH73486	Human sin
15	257	12.8	268	2 AAB87257	Human sin
16	250.6	12.5	251	2 AAX11014	Human bia
17	159	8.0	394	4 AAD04975	5' end of
18	158.4	7.9	160	3 AAC18914	Human sec
19	139	7.0	139	4 AAI56717	Probe #25
20	139	7.0	139	4 ABA40615	Probe #19
21	139	7.0	139	6 ABA24206	Human gen

ALIGNMENTS

RESULT 1
AAL51049

ID AAL51049 standard; DNA; 16449 BP.

AC AAL51049;

DT 20-FEB-2003 (first entry)

Human P2X-like purinergic receptor G-protein coupled receptor gene.

Human; gene; ds; gene therapy; G-protein coupled receptor; chromosome 22;
P2X-like purinergic receptor; anaplastic oligodendroglioma; GPCR;
chronic lymphocytic leukaemia; lung carcinoma; colon carcinoma;
brain carcinoma; drug screening; tissue typing; pharmacogenomic analysis;
SNP; single nucleotide polymorphism.

OS Homo sapiens.

Key	Location/Qualifiers
variation	/tag= a
variation	/note= "Single nucleotide polymorphism"
variation	/tag= b
variation	/note= "Single nucleotide polymorphism"
variation	/tag= c
variation	/note= "Single nucleotide polymorphism"
variation	/tag= d
variation	/note= "Single nucleotide polymorphism"
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	/tag= e
	/product= "Human P2X-like purinergic receptor-related G-protein coupled receptor"
exon	2040..2095
	/tag= f
	/number= 1
intron	2096..2776
	/tag= g
	/number= 1
variation	/tag= h
	/note= "Single nucleotide polymorphism"

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24	120.6	6.0	121	12	ADK92992	Adk92992 Polynucle	
25	120.6	6.0	121	12	ADK92994	Adk92994 Polynucle	
C	26	109.6	5.5	1356	5	AAS78404	Aas78404 DNA encod
27	103.2	5.2	88191	8	ABX14763	Abx14763 Genomic D	
28	102.2	5.1	285	5	ABA18022	Abal8022 Human ner	
29	102.2	5.1	285	5	ABA18019	Abal8019 Human ner	
C	30	102	5.1	52616	4	AAK70459	Aak70459 Human imm
C	31	102	5.1	52616	4	AAK78930	Aak78930 Human imm
C	32	102	5.1	304905	11	ADP75180	Adp75180 Human End
C	33	101.8	5.1	2136	4	AAK72074	Aak72074 Human imm
C	34	101.8	5.1	2136	4	AAK72073	Aak72073 Human imm
C	35	101.2	5.1	24908	4	AAK81665	Aak81665 Human imm
C	36	99	5.0	18902	8	ABZ73865	Abz73865 Secreted
37	99	5.0	18902	10	ABZ67444	Abz67444 Human sec	
38	98.2	4.9	80928	12	ADO25290	Ado25290 Human pro	
C	39	98	4.9	335	2	AAQ59473	Aaq59473 Human bra
40	97.4	4.9	602	4	AAAL06845	Aal06845 Human rep	
41	97.4	4.9	53000	8	AAD55325	Aad55325 Human pro	
42	97.4	4.9	139308	8	ADB12769	Adb12769 Human PRX	
C	43	97.2	4.9	32190	4	AAS36709	Aas36709 Human car
C	44	97.2	4.9	32190	10	ADA47403	Ada47403 Human car
45	96.8	4.8	15870	5	ABA16129	Abal6129 Human ner	

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	TCTCCAAGTCCATGGTGCCTGGTGGTAGGAGACAGGGGGATGAATGTGAACCCCTGATGGC	60
Qy	61	TATAGCCACCTGCCCTCCCTCCCTGCCCTGCATCACTACCTGCCTATTTTGGCTCTAG	120
Db	61	TATAGCCACCTGCCCTCCCTCCCTGCCCTGCATCACTACCTGCCTATTTTGGCTCTAG	120
Qy	121	AAGCTAGTCTCCTATAGTCTCTTAGGACCACTGCCCGCATATGACAGATAAGAACTGA	180
Db	121	AAGCTAGTCTCCTATAGTCTCTTAGGACCACTGCCCGCATATGACAGATAAGAACTGA	180
Qy	181	GGCTAAGGCAACGCAAACTTTTCCCTAAAGTCTACACAGCTGTCAAAAGAAAGCTGGACA	240
Db	181	GGCTAAGGCAACGCAAACTTTTCCCTAAAGTCTACACAGCTGTCAAAAGAAAGCTGGACA	240
Qy	241	ACCTCGGCAACATAGCAGATGATAAAATTAATTAATTAAGCAGATGTGGTAGCCCTCG	300
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Qy	301	TAGTCTCAGGACTCAGAGGCTGAGGAGGCTCACCAGGCTCACCAGTGCAGATTTCAAGAT	360
Db	301	TAGTCTCAGGACTCAGAGGCTGAGGAGGCTCACCAGGCTCACCAGTGCAGATTTCAAGAT	360
Qy	361	GCAGTGAGCTATGATCTCCGCACTGCATGAAAGCTGGGTGACAGAGCAAGACCTGGCT	420
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Qy	421	CTAATAATGAATACATAAAGTCTCAGAGTGTAGTGGTAGCTTAATCTGCCAGAGTCAAGC	480
Db	421	CTAATAATGAATACATAAAGTCTCAGAGTGTAGTGGTAGCTTAATCTGCCAGAGTCAAGC	480
Qy	481	CTCTACCTGTCTGATGACAAATGGCACACTATGCTTTTAACTGATTCAGAGCACCAAA	540
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Qy	541	TGTTTTGTGAATATTTTCCAGGAGAAAAACCGGAAGTAGTTCTAAATTTCTATACATCC	600
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Qy	601	ATTATATTAGTTTACCTGTGGATGGGAAACCCAGCTCTGATGTCAATTCAGGGGGG	660
Db	601	ATTATATTAGTTTACCTGTGGATGGGAAACCCAGCTCTGATGTCAATTCAGGGGGG	660
Qy	661	ACAGCTTTGTGCACTGTCTGGCGGATTTTCAATTTTAACTCTTCTAGAAAGCGCT	720
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Qy	721	TCTCATGTAAAGTTCTGTATGCCCGCAGAGCGCCGAGAGAGGCGAGGGGCTGGAGA	780
Db	721	TCTCATGTAAAGTTCTGTATGCCCGCAGAGCGCCGAGAGAGGCGAGGGGCTGGAGA	780
Qy	781	CGCCCGCAGAGGGCTACGTGCTCTGCTGGACAGAGGTCTCTGCTCTCTCGCGGGCC	840
Db	781	CGCCCGCAGAGGGCTACGTGCTCTGCTGGACAGAGGTCTCTGCTCTCTCGCGGGCC	840
Qy	841	AGCCCACTCCACAAACCCCTCGGGAGAACCCCAAGGGGAGAGACGGGCTGGCCC	900
Db	841	AGCCCACTCCACAAACCCCTCGGGAGAACCCCAAGGGGAGAGACGGGCTGGCCC	900
Qy	901	CTGCCCCGAGCACCTTCCTCTAGTCTGAGTCTGAGTCTGATCGGCTTGGACCTGCTTG	960
Db	901	CTGCCCCGAGCACCTTCCTCTAGTCTGAGTCTGAGTCTGATCGGCTTGGACCTGCTTG	960
Qy	961	GCTTCGGGACCCCTGCAAGAGCTCCACAGGCGCGCTCGCTCTTCTCTCTGCTTTTAA	1020
Db	961	GCTTCGGGACCCCTGCAAGAGCTCCACAGGCGCGCTCGCTCTTCTCTCTGCTTTTAA	1020
Qy	1021	TCCTCCCGAGACTCTGGAGAGAACCGCTCATGTTAGCCCTCTTTCGACGCTCAGACC	1080
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Qy	1081	CTGAGCGGAGACCGCTTGGCGCTCCTTACCTTAGAGCGCGACCCCGGGATGTGGCGGAGTC	1140
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Qy	1141	TGCGGCTGCCTCAGCAATCGAGTGTGGGCTCCATCGACTGGGCTCTGCACCGCAATTA	1200
Db	1141	TGCGGCTGCCTCAGCAATCGAGTGTGGGCTCCATCGACTGGGCTCTGCACCGCAATTA	1200
Qy	1201	GCAGCGGCTCCCCCGGGCGGTGCGCCCGGCAACCACTGCTGTAGTGTGGCTAGAAA	1260
Db	1201	GCAGCGGCTCCCCCGGGCGGTGCGCCCGGCAACCACTGCTGTAGTGTGGCTAGAAA	1260
Qy	1261	CCGTGGCTCTCCTGCGCTGAGGCTCCTGCGCTCAGAGGATAAACTGCACGCGCAGGGC	1320
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Qy	1321	TATGCACTGGGCTGGGCGCTTGTGGCACTCCTCCTGCTCTTCTAGGGGTTCCAGCAT	1380
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Qy	1381	CGCCCCCTTTCTGGACTGGGAAACACGCTGACTCCAGGACTTGTGTCTCTCACTG	1440
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Qy	1441	CACTGGGGAAGTGGGCGGGCAGCTTTTTCAGGAGGGCTTGGGGAATTCGCGAGAGCCAG	1500
Db	1441	CACTGGGGAAGTGGGCGGGCAGCTTTTTCAGGAGGGCTTGGGGAATTCGCGAGAGCCAG	1500
Qy	1501	GTCAACCTCTCACTCTGTGGCTCTTAGTTATCTTGTGATGCTCTGGTCTTGTGATAGCTG	1560
Db	1501	GTCAACCTCTCACTCTGTGGCTCTTAGTTATCTTGTGATGCTCTGGTCTTGTGATAGCTG	1560
Qy	1561	CTCCCTGCAACAGGAACCTCCATCCCATCTTTTGTCTGTGTCGAATTCAGAAATCTG	1620
Db	1561	CTCCCTGCAACAGGAACCTCCATCCCATCTTTTGTCTGTGTCGAATTCAGAAATCTG	1620
Qy	1621	CAAGGCTAGCTTAGAGTCACTTTTCCGGAGAGTTTCTCAACACCTTCCCGGCCCTG	1680
Db	1621	CAAGGCTAGCTTAGAGTCACTTTTCCGGAGAGTTTCTCAACACCTTCCCGGCCCTG	1680
Qy	1681	CTGCTCTGCCCTCAGGCCCTCTCTCAGACACTGATTAACAGCTCTCGTCTCCACCT	1740
Db	1681	CTGCTCTGCCCTCAGGCCCTCTCTCAGACACTGATTAACAGCTCTCGTCTCCACCT	1740
Qy	1741	CCACACCTTCCACTCCACCCAGGAAGTGAAGCCAGAGGCGAGGAGCAGAGCTCTGC	1800
Db	1741	CCACACCTTCCACTCCACCCAGGAAGTGAAGCCAGAGGCGAGGAGCAGAGCTCTGC	1800
Qy	1801	TGTTCTCTGTGTCAGAGGCGCCAGCAAGGGAATGTAGGAGGCTGGAGGTGCAGGCA	1860
Db	1801	TGTTCTCTGTGTCAGAGGCGCCAGCAAGGGAATGTAGGAGGCTGGAGGTGCAGGCA	1860
Qy	1861	GCTGGGATTAGGGGTTGAGGGCTGGGTGTGGAGGCTGGATCTGGATCTCTTGTAGTGG	1920
Db	1861	GCTGGGATTAGGGGTTGAGGGCTGGGTGTGGAGGCTGGATCTGGATCTCTTGTAGTGG	1920
Qy	1921	AAGTGTCCCTTTAAAGCAACTGGGCTGGGCTGGGCTGGGCTGGTTCCTCTGCTTC	1980
Db	1921	AAGTGTCCCTTTAAAGCAACTGGGCTGGGCTGGGCTGGGCTGGTTCCTCTGCTTC	1980
Qy	1981	AGCTGCGGCTGCAGTGGCA 2000	
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RESULT 2
AAI18897/c
ID AAI18897 standard; DNA; 563 BP.
XX AAI18897;
XX
DT 12-OCT-2001 (first entry)

XX DE Probe #8830 for gene expression analysis in human cervical cell sample.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer; ss.
XX OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000670.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-489901/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.
XX PS Claim 25; SEQ ID NO 8830; 487pp; English.
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENPs). The present sequence is one such probe. The SENPs are derived
XX CC from human HeLa cells. The SENPs can be used to produce a single exon
XX CC microarray, which can be used for measuring human gene expression in a
XX CC sample derived from human cervical epithelial cells. By measuring gene
XX CC expression, the probes are therefore useful in grading and/or staging of
XX CC diseases of the cervix, notably cervical cancer. Note: The sequence data
XX CC for this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 563 BP; 129 A; 148 C; 156 G; 130 T; 0 U; 0 Other;
Query Match 28.1%; Score 563; DB 4; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.7e-139;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 386 CACTGAAAGCTGGGTGACAGAGCAAGACCTGGCTCTAATAATGAATACATAAAGTCTC 445
Db 563 CACTGAAAGCTGGGTGACAGAGCAAGACCTGGCTCTAATAATGAATACATAAAGTCTC 504
QY 446 ACAGCTAGTGTAGCTAATCCTGCCAGAGTCAGGCTCTACCTGTCTGATGACAAATGGC 505
Db 503 ACAGCTAGTGTAGCTAATCCTGCCAGAGTCAGGCTCTACCTGTCTGATGACAAATGGC 444
QY 506 ACACATGTCTTTTAACTGATTCAGACCAACAAATGTTTGTGAATATTTTCCCGAGG 565
Db 443 ACACATGTCTTTTAACTGATTCAGACCAACAAATGTTTGTGAATATTTTCCCGAGG 384
QY 566 AAAAAACCGGAAGTAGTCTTAATCTTATACATCCATTATAGTTTACCTGTGGATT 625
Db 383 AAAAAACCGGAAGTAGTCTTAATCTTATACATCCATTATAGTTTACCTGTGGATT 324
QY 626 GGGAAAAACCCAGCTCTGATTCGATTCAGGCGGGACAGCCTTTGGTGCACTGTCTGGCG 695
Db 323 GGGAAAAACCCAGCTCTGATTCGATTCAGGCGGGACAGCCTTTGGTGCACTGTCTGGCG 264
QY 686 GGATTTTCCATTTTAACTCTTACAGGCGCTTCTCATGTCTTAAGTTCCCTGATGCGG 745
Db 263 GGATTTTCCATTTTAACTCTTACAGGCGCTTCTCATGTCTTAAGTTCCCTGATGCGG 204

QY 746 CCAGGAGCGCCGAGAGAGAGGGGCTGGAGAGCGCCCGCAGAGGGCTACCTGCCT 805
Db 203 CCAGGAGCGCCGAGAGAGAGGGGCTGGAGAGCGCCCGCAGAGGGCTACCTGCCT 144
QY 806 GCTGACACAGAGTCTCTCTGCTCTCTCTGCGCGGCGGACCCACCTCCACAAACCCCTGCG 865
Db 143 GCTGACACAGAGTCTCTCTGCTCTCTCTGCGCGGCGGACCCACCTCCACAAACCCCTGCG 84
QY 866 GAGAAAGCCCCCAAGGGGAGAGAGCGGCTGCGCGGCGGCTGCGCGGCGGCTGCGCGGCTGCG 925
Db 83 GAGAAAGCCCCCAAGGGGAGAGAGCGGCTGCGCGGCGGCTGCGCGGCGGCTGCGCGGCTGCG 24
QY 926 GGTGGAGTCTGAATCGGCTTG 948
Db 23 GGTGGAGTCTGAATCGGCTTG 1
RESULT 3
ABA63896/c
ID ABA63896 standard; DNA; 563 BP.
XX AC ABA63896;
XX XX
XX DT 01-FEB-2002 (first entry)
XX DE Human foetal liver single exon nucleic acid probe #12201.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX XX Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-483447/52.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human foetal liver.
XX PS Claim 1; SEQ ID NO 12201; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human foetal liver. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 563 BP; 129 A; 148 C; 156 G; 130 T; 0 U; 0 Other;
Query Match 28.1%; Score 563; DB 4; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.7e-139;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 386 CACTGAAAGCTGGGTGACAGAGCAAGACCTGGCTCTAATAATGAATACATAAAGTCTC 445

XX OS Homo sapiens.
 XX PN WO200157274-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000666.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX XX WPI; 2001-488999/53.
 XX DR Single exon nucleic acid probes for analyzing gene expression in human hearts.
 XX PT Claim 1; SEQ ID NO 9542; 530pp; English.
 XX PS The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart, and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 563 BP; 129 A; 148 C; 156 G; 130 T; 0 U; 0 Other;
 Query Match 28.1%; Score 563; DB 4; Length 563;
 Best Local Similarity 100.0%; Pred. No. 1.7e-139;
 Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 CACTGAAGCTGGGTGACAGAGCAGACCCCTGGCTCTAATAAATGAATACATAAAGTCTC 445
 DB 563 CACTGAAGCTGGGTGACAGAGCAGACCCCTGGCTCTAATAAATGAATACATAAAGTCTC 504

QY 446 ACAGCTAGTGGTAGCTAATCTGCGCAGAGTCAGGCCTCTACCTGTCTGATGACAAATGGC 505
 DB 503 ACAGCTAGTGGTAGCTAATCTGCGCAGAGTCAGGCCTCTACCTGTCTGATGACAAATGGC 444

QY 506 ACACATATGCTTTAACTGATTCGACACCAAAATGTTTGTGAATATTTTCCCGAGG 565
 DB 443 ACACATATGCTTTAACTGATTCGACACCAAAATGTTTGTGAATATTTTCCCGAGG 384

QY 566 AAAAAACCGAAGTAGTCTTAAATCTATACATCCATTATATTAGTTTACCTGTGGATT 625
 DB 393 AAAAAACCGAAGTAGTCTTAAATCTATACATCCATTATATTAGTTTACCTGTGGATT 324

QY 626 GGGAAAAACCGAGCTCTGATTCGATTCAGGGCGGAGCAGCCTTTGGTGCACTGTCTGGG 685
 DB 323 GGGAAAAACCGAGCTCTGATTCGATTCAGGGCGGAGCAGCCTTTGGTGCACTGTCTGGG 264

QY 686 GGATTTTCCATTTTAACTCTCTAGAAAGGCGCTTCTCATGGTAAAGTTTCCCTGATCCG 745
 DB 263 GGATTTTCCATTTTAACTCTCTAGAAAGGCGCTTCTCATGGTAAAGTTTCCCTGATCCG 204

QY 746 CCAGAGCGCGAGAGAGGCGAGGGGCTGGAGACGCCCGCGCAGAGGGGTACGTGCGCT 805
 DB 203 CCAGAGCGCGAGAGAGGCGAGGGGCTGGAGACGCCCGCGCAGAGGGGTACGTGCGCT 144

QY 806 GTTGACAGAGGTCTCTGCTCTCTCTGCGGCGGCGCAGCCACCTCCACAAACCCCTGCGG 865
 DB 143 GTTGACAGAGGTCTCTGCTCTCTCTGCGGCGGCGCAGCCACCTCCACAAACCCCTGCGG 84

QY 866 GAGAGCCCCCAAGGAGGAGGAGCGGCTGCGCCCTGCGGAGCAGCTTCCGCTCTCTA 925
 DB 83 GAGAGCCCCCAAGGAGGAGGAGCGGCTGCGCCCTGCGGAGCAGCTTCCGCTCTCTA 24

QY 926 GGTGAGGTCTGAATCGGCCTTG 948
 DB 23 GGTGAGGTCTGAATCGGCCTTG 1

RESULT 6

AAK38120/c
 ID AAK38120 standard; DNA; 563 BP.
 XX AAK38120;
 XX AC AAK38120;
 XX XX
 XX 06-NOV-2001 (first entry)
 XX DE Human bone marrow expressed single exon probe SEQ ID NO: 12677.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
 XX OS Homo sapiens.
 XX PN WO200157276-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000668.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX XX WPI; 2001-488999/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

Example 4; SEQ ID NO 12677; 658pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention

Sequence 563 BP; 129 A; 148 C; 156 G; 130 T; 0 U; 0 Other;

Query Match 28.1%; Score 563; DB 4; Length 563;

Best Local Similarity 100.0%; Pred. No. 1.7e-139;

Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 CACTGAAGCTGGGTGACAGAGCAGACCCCTGGCTCTAATAAATGAATACATAAAGTCTC 445

DB 563 CACTGAAGCTGGGTGACAGAGCAGACCCCTGGCTCTAATAAATGAATACATAAAGTCTC 504

QY 446 ACAGCTAGTGGTAGCTAATCTGCGCAGAGTCAGGCCTCTACCTGTCTGATGACAAATGGC 505

Db 503 ACAGCTAGTGTAGTAATCTCTGACAGAGTCTACCTGCTGATGACAAATGGC 444
 Qy 506 ACACATATGCTTTTAACTGATTCAGACACCAAAATGTTTGTGAATTTTCCACGGG 565
 Db 443 ACACATATGCTTTTAACTGATTCAGACACCAAAATGTTTGTGAATTTTCCACGGG 384
 Qy 566 AAAAAACCGGAGTAGTCTTAAATCTATACATCCATTATATAGTTTACCTGTGGATT 625
 Db 383 AAAAAACCGGAGTAGTCTTAAATCTATACATCCATTATATAGTTTACCTGTGGATT 324
 Qy 626 GGGAAAAACCGAGCTCTGATTCGATTTAGGGGGGAGACGCTTTGGTGCACATGCTGGCG 685
 Db 323 GGGAAAAACCGAGCTCTGATTCGATTTAGGGGGGAGACGCTTTGGTGCACATGCTGGCG 264
 Qy 686 GGATTTTTCATTTTAACTCTCTCTAGAGGCGCTTCTCATGGTAAAGTCTCTGATGCG 745
 Db 263 GGATTTTTCATTTTAACTCTCTCTAGAGGCGCTTCTCATGGTAAAGTCTCTGATGCG 204
 Qy 746 CCAGAGCGCCGAGGAGGCGAGGGGCTGGAGACGCGCCCGCAGAGGGCTACGTGCCCT 805
 Db 203 CCAGAGCGCCGAGGAGGCGAGGGGCTGGAGACGCGCCCGCAGAGGGCTACGTGCCCT 144
 Qy 806 GGTGACACAGAGTCTCTCTGCTCTCTGCGGGGCGGCGAGCGGCTCCGACACCCCTGGG 865
 Db 143 GGTGACACAGAGTCTCTCTGCTCTCTGCGGGGCGGCGAGCGGCTCCGACACCCCTGGG 84
 Qy 866 GAGAAAGCCCCAAGGGAGGAGACGGGCTGGCCCTGCGCCCTGCGCCCTGCGCTCTCTA 925
 Db 83 GAGAAAGCCCCAAGGGAGGAGACGGGCTGGCCCTGCGCCCTGCGCCCTGCGCTCTCTA 24
 Qy 926 GGTGAGTCTGAATCGGCTTG 948
 Db 23 GGTGAGTCTGAATCGGCTTG 1

RESULT 7

AAK12404/c
 ID AAK12404 standard; DNA; 563 BP.
 AC AAK12404;
 XX
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe SEQ ID NO: 12395.
 XX
 KW Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW ss.
 OS Homo sapiens.
 XX
 XX WO200157275-A2.
 PN
 PD 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000667.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-483446/52.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.

XX Example 4; SEQ ID NO 12395; 650pp + Sequence Listing; English.
 PS

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention

XX SQ Sequence 563 BP; 129 A; 148 C; 156 G; 130 T; 0 U; 0 Other;

Query Match 28.1%; Score 563; DB 4; Length 563;

Best Local Similarity 100.0%; Pred. No. 1.7e-139;

Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 CACTGAAAGCTGGGTGACAGAGCAAGACCTGTGCTTAATAATGAATACATAAAGTCTC 445
 Db 563 CACTGAAAGCTGGGTGACAGAGCAAGACCTGTGCTTAATAATGAATACATAAAGTCTC 504
 Qy 446 ACAGCTAGTGTAGTAAATCTGCCAGAGTCTACCTGTCTGATGACAAATGGC 505
 Db 503 ACAGCTAGTGTAGTAAATCTGCCAGAGTCTACCTGTCTGATGACAAATGGC 444
 Qy 506 ACATATGCTTTTAACTGATTCAGACACCAAAATGTTTGTGAATATTTTCCACGGG 565
 Db 443 ACATATGCTTTTAACTGATTCAGACACCAAAATGTTTGTGAATATTTTCCACGGG 384
 Qy 566 AAAAAACCGGAGTAGTCTTAAATCTATACATCCATTATATAGTTTACCTGTGGATT 625
 Db 383 AAAAAACCGGAGTAGTCTTAAATCTATACATCCATTATATAGTTTACCTGTGGATT 324
 Qy 626 GGGAAAAACCGAGCTCTGATTCGATTTAGGGGGGAGACGCTTTGGTGCACATGCTGGCG 685
 Db 323 GGGAAAAACCGAGCTCTGATTCGATTTAGGGGGGAGACGCTTTGGTGCACATGCTGGCG 264
 Qy 686 GGATTTTTCATTTTAACTCTCTCTAGAGGCGCTTCTCATGGTAAAGTCTCTGATGCGG 745
 Db 263 GGATTTTTCATTTTAACTCTCTCTAGAGGCGCTTCTCATGGTAAAGTCTCTGATGCGG 204
 Qy 746 CCAGAGCGCCGAGGAGGCGGAGGCGGCTGGAGACGCGCCCGCAGAGGGCTACGTGCCCT 805
 Db 203 CCAGAGCGCCGAGGAGGCGGAGGCGGCTGGAGACGCGCCCGCAGAGGGCTACGTGCCCT 144
 Qy 806 GCTGGAACAGAGTCTCTCTGCTCTCTGCGGGGCGGCGAGCGGCTCCGACACCCCTGGG 865
 Db 143 GCTGGAACAGAGTCTCTCTGCTCTCTGCGGGGCGGCGAGCGGCTCCGACACCCCTGGG 84
 Qy 866 GAGAAAGCCCCAAGGGAGGAGACGGGCTGGCCCTGCGCCCTGCGCCCTGCGCTCTCTA 925
 Db 83 GAGAAAGCCCCAAGGGAGGAGACGGGCTGGCCCTGCGCCCTGCGCCCTGCGCTCTCTA 24
 Qy 926 GGTGAGTCTGAATCGGCTTG 948
 Db 23 GGTGAGTCTGAATCGGCTTG 1

RESULT 8

ABS37739/c

ID ABS37739 standard; DNA; 563 BP.

XX

AC ABS37739;

XX

DT 25-FEB-2003 (first entry)

XX Human liver single exon probe, SEQ ID No 12729.

DE

KW Human; single exon nucleic acid probe; liver; cirrhosis;

KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;

KW coronary heart disease; ss.

XX Homo sapiens.

OS

XX PN W0200157273-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX XX WPI; 2001-488898/53.
 XX DT Human genome-derived single exon nucleic acid probes useful for analyzing
 XX PT gene expression in human adult liver.
 XX DE Human genome-derived single exon probe from lung SEQ ID No 12130.
 XX XX
 XX PS Claim 1; SEQ ID NO 12729; 658pp; English.
 XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. AB825011-AB851005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 563 BP; 129 A; 148 C; 156 G; 130 T; 0 U; 0 Other;
 Query Match 28.1%; Score 563; DB 4; Length 563;
 Best Local Similarity 100.0%; Pred. NO. 1.7e-139;
 Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 386 CACTGAAGCTGGGTGACAGACGACGACCCCTGGCTCTAATAAATGAATACATAAAGTCTC 445
 DB 563 CACTGAAGCTGGGTGACAGACGACGACCCCTGGCTCTAATAAATGAATACATAAAGTCTC 504
 QY 446 ACAGCTAGTGTAGCTAATCTGCCAGAGTCAGGCTCTACCTGTCTGTGATGACAAATGCC 505
 DB 503 ACAGCTAGTGTAGCTAATCTGCCAGAGTCAGGCTCTACCTGTCTGTGATGACAAATGCC 444
 QY 506 ACATCTATGCTTTTAACTGATTCAGACCAACAAATGTTTGTGAATATTTTCCCGAGG 565
 DB 443 ACATCTATGCTTTTAACTGATTCAGACCAACAAATGTTTGTGAATATTTTCCCGAGG 384
 QY 566 AAAAAACCGGAAGTAGTCTTAAATCTATATCATCCATATATAGTTTACCTGTGGATT 625
 DB 383 AAAAAACCGGAAGTAGTCTTAAATCTATATCATCCATATATAGTTTACCTGTGGATT 324
 QY 626 GGGAAACCCAGCTCTGATTCATTCAGGCGGAGCAGCTTGTGGTCACTCTCTGGCG 685
 DB 323 GGGAAACCCAGCTCTGATTCATTCAGGCGGAGCAGCTTGTGGTCACTCTCTGGCG 264
 QY 686 GGATTTTCCATTTTAACTCTCTTAGAAGCGCTTCTCATGTGTAAGTTCTCTGATGCCG 745
 DB 263 GGAATTTTCCATTTTAACTCTCTTAGAAGCGCTTCTCATGTGTAAGTTCTCTGATGCCG 204
 QY 746 CCAGGAGCGCGAGAGGCGGCGGCTGGAGACGCCCGCAGAGGGCTAGTGCCTT 805

DB 203 CCAGGAGCGCCGAGGAGGAGGCGGCGCTGGAGACGCGCCGCGAGAGGCTACGTGCCT 144
 QY 806 GCTGACAGAGTCTCTCTCCCTCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 865
 DB 143 GCTGACAGAGTCTCTCTCCCTCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 84
 QY 866 GAGAAAGCCCCCAAGGAGGAGGAGGAGGCGGCTGGCGGCTGGCGGCGGCGGCGGCGGCGG 925
 DB 83 GAGAAAGCCCCCAAGGAGGAGGAGGAGGCGGCTGGCGGCTGGCGGCGGCGGCGGCGGCGG 24
 QY 926 GGTGAGAGTCTCAATCGGCGCTTG 948
 DB 23 GGTGAGAGTCTCAATCGGCGCTTG 1
 RESULT 9
 ABS12139/c
 ID ABS12139 standard; DNA; 563 BP.
 XX XX
 XX AC ABS12139;
 XX XX
 XX DT 19-AUG-2002 (first entry)
 XX XX
 XX DE Human genome-derived single exon probe from lung SEQ ID No 12130.
 XX XX
 XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX KW
 OS Homo sapiens.
 XX XX
 XX PN W0200186003-A2.
 XX PD 15-NOV-2001.
 XX XX
 XX PF 30-JAN-2001; 2001WO-US000665.
 XX XX
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX XX
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX XX
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX XX WPI; 2002-114183/15.
 XX DR
 XX PT Spatially-addressable set of single exon nucleic acid probes, used to
 XX PT measure gene expression in human lung samples.
 XX PS Claim 1; SEQ ID NO 12130; 634pp; English.
 XX XX
 XX CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array: identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 563 BP; 129 A; 148 C; 156 G; 130 T; 0 U; 0 Other;

Query Match 28.1%; Score 563; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.7e-139;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 386 CACTCAAGCTGGGTGACAGAGACCCCTGGCTCTAATAATGAATACATAAGTCTC 445
DB 563 CACTCAAGCTGGGTGACAGAGACCCCTGGCTCTAATAATGAATACATAAGTCTC 504
QY 446 ACAGCTAGTGGTAGTAATCTCTGCGAGAGTCAAGGCTCTACTGCTGATGACAAATGGC 505
DB 503 ACAGCTAGTGGTAGTAATCTCTGCGAGAGTCAAGGCTCTACTGCTGATGACAAATGGC 444
QY 506 ACACATATCTCTTTAACTGATGACAGACCAACAAATGTTTGTGAATTTTCCCGAGG 565
DB 443 ACACATATCTCTTTAACTGATGACAGACCAACAAATGTTTGTGAATTTTCCCGAGG 384
QY 566 AAAAAACCGGAGTAGTCTAAATCTATACATCCATTATATTAGTTTACCTCTGGATT 625
DB 383 AAAAAACCGGAGTAGTCTAAATCTATACATCCATTATATTAGTTTACCTCTGGATT 324
QY 626 GGGAAACCCAGCTCTGATTGCAATTCAGGGGGGAGACGCTTTGGTCACTGTCTGGCG 685
DB 323 GGGAAACCCAGCTCTGATTGCAATTCAGGGGGGAGACGCTTTGGTCACTGTCTGGCG 264
QY 686 GGATTTTCCATTTTAACTCTCTCTAGAGGCGCTTCTCATGGTAAAGTTCTCTGATGCG 745
DB 263 GGATTTTCCATTTTAACTCTCTCTAGAGGCGCTTCTCATGGTAAAGTTCTCTGATGCG 204
QY 746 CCAGAGGCGCCGAGAGAGGGGAGGGGCTGAGACGCGCCCGCAGAGGGCTACGTGCCT 805
DB 203 CCAGAGGCGCCGAGAGAGGGGAGGGGCTGAGACGCGCCCGCAGAGGGCTACGTGCCT 144
QY 806 GCTGACAGAGGTCTCTGCTCTCTGCGGCGCCAGCCCTCCACACACCCCTGCGG 865
DB 143 GCTGACAGAGGTCTCTGCTCTCTGCGGCGCCAGCCCTCCACACACCCCTGCGG 84
QY 866 GAGAAAGCCCCAAGGGGAGGAGACGGGCTTGCCCCCTGCGGAGCACTTCCGTCTCTA 925
DB 83 GAGAAAGCCCCAAGGGGAGGAGACGGGCTTGCCCCCTGCGGAGCACTTCCGTCTCTA 24
QY 926 GGTGAGGTCTGAATCGGCTTG 948
DB 23 GGTGAGGTCTGAATCGGCTTG 1

RESULT 10

AAI43912/c
ID AAI43912 standard; DNA; 554 BP.
XX
XX AAI43912;
AC AAI43912;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #12598 used to measure gene expression in human placenta sample.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
XX Homo sapiens.
OS
PN WO200157272-A2.
XX
XX 09-AUG-2001.
PF
XX 30-JAN-2001; 2001WO-US0000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 12598; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 554 BP; 109 A; 170 C; 186 G; 89 T; 0 U; 0 Other;
Query Match 27.7%; Score 554; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 4.2e-137;
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 615 ACCTGTGGATTGGGAAACCCAGCTCTGATTGATTCAGGGCGGACAGCCTTTGGTGC 674
DB 554 ACCTGTGGATTGGGAAACCCAGCTCTGATTGATTCAGGGCGGACAGCCTTTGGTGC 495
QY 675 ACTGTCTGGCGGATTTTCCATTTTAACTCTCTAGAGGCGCTTCTCATGTTAACT 734
DB 494 ACTGTCTGGCGGATTTTCCATTTTAACTCTCTAGAGGCGCTTCTCATGTTAACT 435
QY 735 TCCTGTATCCCGCCAGAGGCGCCGAGGAGAGGGGCTGGAGACGCGCCCGCAGAGGG 794
DB 434 TCCTGTATCCCGCCAGAGGCGCCGAGGAGAGGGGCTGGAGACGCGCCCGCAGAGGG 375
QY 795 CTACGTGCTCTGTGACAGAGTCTCTGCTCTCTGCGGCGCGCAGGCCACCTCCAC 854
DB 374 CTACGTGCTCTGTGACAGAGTCTCTGCTCTCTGCGGCGCGCAGGCCACCTCCAC 315
QY 855 AACCCCTGCGGAGAGCCCGCCAGGAGGAGCGGCTGCGCCCTGCGCGAGCACC 914
DB 314 AACCCCTGCGGAGAGCCCGCCAGGAGGAGCGGCTGCGCCCTGCGCGAGCACC 255

15-NOV-2001.

30-JAN-2001; 2001WO-US000665.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207458P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632386.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 1; SEQ ID NO 12020; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagazer syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 554 BP; 109 A; 170 C; 186 G; 89 T; 0 U; 0 Other;

Query Match	27.7%;	Score 554;	DB 6;	Length 554;
Best Local Similarity	100.0%;	Prod. NO. 4.2e-137;		
Matches 554;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	615	ACTGTGGATTGGGAAACCCAGCTCTCATTTGCATTTTCAGGGGGGACAGCCTTTGGTGC	674	
Db	554	ACTGTGGATTGGGAAACCCAGCTCTCATTTGCATTTTCAGGGGGGACAGCCTTTGGTGC	495	
QY	675	ACTGTGCGGGGATTTTTCATTTTAACTCCTTCTAGAAAGCGCCTTTCTCATGGTAAAGT	734	

494	Db	ACTGTC	TCGGCGG	ATTTTC	CAATTT	TAACCT	CTCTT	AGAG	CGCC	TTCT	CATG	TTAA	AGT	435						
735	Qy	TCCTG	ATGCCG	CAGAG	CGCCG	AGAG	AGGG	CAG	GGG	CTG	GAG	AGCG	CCCG	CAGAGG	794					
434	Db	TCCTG	ATGCCG	CAGAG	CGCCG	AGAG	AGGG	CAG	GGG	CTG	GAG	AGCG	CCCG	CAGAGG	375					
795	Qy	CTACG	TGCC	CTG	CTG	GAC	AGAG	TCT	CTG	CTCT	TCG	CGG	CGC	CAG	CCCA	CTCC	CAC	854		
374	Db	CTACG	TGCC	CTG	CTG	GAC	AGAG	TCT	CTG	CTCT	TCG	CGG	CGC	CAG	CCCA	CTCC	CAC	315		
855	Qy	AACCC	CTGGG	GAG	AGCCCC	CAAGG	GAG	GAC	CGG	CTG	CGCC	CTG	CGCC	CTG	CGCC	CTG	CGCC	914		
314	Db	AACCC	CTGGG	GAG	AGCCCC	CAAGG	GAG	GAC	CGG	CTG	CGCC	CTG	CGCC	CTG	CGCC	CTG	CGCC	255		
915	Qy	TTCCG	CTCT	AGT	CGG	AGT	CTGA	ATCG	GGC	CTT	GGG	AC	CCT	TGCT	TGG	CTT	CGG	974		
254	Db	TTCCG	CTCT	AGT	CGG	AGT	CTGA	ATCG	GGC	CTT	GGG	AC	CCT	TGCT	TGG	CTT	CGG	195		
975	Qy	TGCA	AGCT	CTCA	AGCG	CGCG	CTG	CGCT	TTCC	TCT	CGT	TTTT	TA	TCCT	CCCG	AC	CACT	1034		
194	Db	TGCA	AGCT	CTCA	AGCG	CGCG	CTG	CGCT	TTCC	TCT	CGT	TTTT	TA	TCCT	CCCG	AC	CACT	135		
1035	Qy	CTGG	CAGG	ACCG	CTCAT	CGTT	ACG	CCCT	TTTC	GAC	CCCT	CAG	AC	CTG	AGG	CGG	AGAC	1094		
134	Db	CTGG	CAGG	ACCG	CTCAT	CGTT	ACG	CCCT	TTTC	GAC	CCCT	CAG	AC	CTG	AGG	CGG	AGAC	75		
1095	Qy	GC	TTGG	CGC	CTCA	CTT	AGAG	CGCG	AC	CCG	GGG	ATG	TGG	GCG	GA	TG	CGG	CTGC	GTGA	1154
74	Db	GC	TTGG	CGC	CTCA	CTT	AGAG	CGCG	AC	CCG	GGG	ATG	TGG	GCG	GA	TG	CGG	CTGC	GTGA	15
1155	Qy	CCA	ATCG	AGT	GTGG	1168														
14	Db	CCA	ATCG	AGT	GTGG	1														

RESULT 13
ADA53808/c
ID ADA53808 standard; cDNA; 1904 BP.
XX XX
AC AC
ADA53808;
XX XX
DT 20-NOV-2003 (first entry)
XX XX
XX XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
XX inflammatory disease; osteoporosis; neurological disease; gene; ss.
XX Homo sapiens.

RESULT 13

ADA53808/c
ID ADA53808 standard; cDNA; 1904 BP.

AC ADA53808:

XX
DT 20-NOV-2003 (first entry)

XX DE Human coding sequence. SEQ ID 1376.

Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease; gene; ss.

XX
OS Homo sapiens.

XX
PN
EP1293569-A2

XX
PD 19-MAR-2003

XX
PF 21-MAR-2002. 2002EP-00006586XX
14-SEP-2001. 2001.TP-00328381

PR 24-JAN-2002; 2002US-0350435P.
YY

PA (HELI-) HELIX RES INST.
PA (HELI-) HELIX RES INST.
PA (HELI-) HELIX RES INST.

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PI Yamamoto J, Isono Y, Hio Y, Otsuka
PI coki N yaschikawa
PI

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DR P-PSDB; ADA55447.

PT New polynucleotides encoding full

Db 237 CACTGATACAGCTGCTCTCCCATCTCTCACACAGTCCACTCCACCGGAGAGTG 296
QY 1772 AGGCCAGAGGCGAGGACAGAGCTGCTGCTGCTTCTCTGTGTGCGAGGCGCCAGCAAGGG 1831
Db 297 AGGCCAGAGGCGAGGACAGAGCTGCTGCTGCTTCTCTGTGTGCGAGGCGCCAGCAAGAG 356
QY 1832 AATGTAGGAGGCTGGGAGGTCAGGCGAGCTGGGATTAGGGTTGAGGGTGGGCTGTTG 1891
Db 357 AATGTAGGAGGCTGGGAGGTCAGGCGAGCTGGGATTAGGGTTGAGGGTGGGCTGTTG 416
QY 1892 GAGGCTGAGCTGAGTCCCTGCTTTAGTGAAGTGTCCCTTTAAACAGCAACTGGCCTGGCC 1951
Db 417 GAGG-----CTGGATCCTGCTTTAGTGAAGTGTCCCTTTAAACAGCGGCTGGGCTGGCC 470
QY 1952 TGGCTCGGGCCCTGCTTTGCTCTCTCTGTCACCTGGGC 1989
Db 471 TGGCTCGGGCCCTGCTTTGCTCTCTCTGTCACCTGGGC 508

RESULT 15
AAH87257/C
ID AAH87257 standard; DNA; 268 BP.
XX AC AAH87257;
XX AC
DT 27-FEB-2002 (first entry)
XX DE Human single nucleotide polymorphism containing DNA sequence #2114.
XX KW Biallelic marker; polymorphism; human; disease; diagnosis; treatment;
KW phenotypic trait; gene therapy; forensic; paternity; mapping; cancer;
KW transgenic; single nucleotide polymorphism; SNP; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT variation replace(60,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX WO9953095-A2.
XX PD 21-OCT-1999.
XX PF 30-MAR-1999; 99WO-US006893.
XX PR 09-APR-1998; 98US-00057871.
XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX PI Lander ES, Wang D, Hudson T;
XX PS WPI; 1999-620443/53.
XX PT Polymorphic human genomic sequences and related allele-specific probes
PT and primers, useful for genetic analysis, e.g. diagnosis and monitoring
PT of disease.
XX PS
XX PS Claim 1; Page 263; 330pp; English.

XX CC This invention describes novel human nucleic acid segments (I) containing
XX polymorphic sites. The polynucleotides of (I) are used for, e.g.
XX correlating disease polymorphisms (or disease susceptibility) or other
XX phenotypic traits (e.g. baldness, obesity, fertility, strength, response
XX to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation,
XX heart or central nervous system diseases; detecting susceptibility to
XX microbial infection; treating or preventing such diseases; forensic
XX analysis; gene therapy; paternity testing; mapping genomic loci
XX associated with phenotypic traits (and subsequent cloning of the genes
XX responsible); and the production of transgenic organisms. Antibodies
XX raised against (I) are useful as diagnostic and therapeutic tools and in
XX drug screening. AAH85144 - AAH87644 represent the human DNA sequences

CC containing biallelic polymorphic sites described in the invention
XX
SQ Sequence 268 BP; 75 A; 55 C; 56 G; 82 T; 0 U; 0 Other;
Query Match 12.8%; Score 257; DB 2; Length 268;
Best Local Similarity 99.6%; Pred. No. 4.2e-58;
Matches 268; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 364 GTGAGCTATGATCCTGCCACTGCACCTGAAAGCTGGGTGACAGCAAGACCCCTGGCTCTA 423
Db 268 GTGAGCTATGATCCTGCCACTGCACCTGAAAGCTGGGTGACAGCAAGACCCCTGGCTCTA 209
QY 424 ATAAATGAATACATAAAGTCTCACAGCTAGTGGTAGCTAATCTCGCAGAGTCAGGCCTC 483
Db 208 ATAAATGAATACATAAAGTCTCACAGCTAGTGGTAGCTAATCTCGCAGAGTCAGGCCTC 149
QY 484 TACCTGCTGATGACAAATGGCACACTATGCTTTTAACTGATTGCAGACCAAAATGT 543
Db 148 TACCTGCTGATGACAAATGGCACACTATGCTTTTAACTGATTGCAGACCAAAATGT 89
QY 544 TTTGTGAATATTTTCCCGAGGGAATAAACCGGAAGTAGTTCTAAATTTATATCATCATT 603
Db 88 TTTGTGAATATTTTCCCGAGGGAATAAACCGGAAGTAGTTCTAAATTTATATCATCATT 30
QY 604 ATATTAGTTTACCTGTGGATTGGGAAAA 632
Db 29 ATATTAGTTTACCTGTGGATTGGGAAAA 1

Search completed: November 21, 2004, 18:28:54
Job time : 971.553 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 12:30:45 ; Search time 3207.1 Seconds
(without alignments)
11373.559 Million cell updates/sec

Title: US-09-820-095B-3_COPY_10000_11000
Perfect score: 1001
Sequence: 1 acacagtcacottcgcaag.....tgggtttcaccaattgtggc 1001

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_gss1:*
8: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154.8	15.5	2191	3	BC047287 Homo sapi
2	154.4	15.4	353	2	AW451665 UI-H-Bi3-
3	153.4	15.3	733	4	BI753477 603026391
4	152.6	15.2	292	1	AI703080 wd81f03.x
5	152.4	15.2	525	8	B56395 CIT-HSP-200
6	152.2	15.2	414	5	BX504814 DKFZp686J
7	152.2	15.2	681	9	AG059520 Pan trogl
8	151.6	15.1	954	5	BQ231446 AGENCOURT
9	151.2	15.1	1150	4	BM807563 AGENCOURT
10	151.1	15.1	618	2	BF680805 602156044
11	150.8	15.1	322	1	AA331580 nj65a07.s
12	150.6	15.1	664	5	BQ005623 UI-H-EB0-
13	150.6	15.0	803	8	BZ601931 WHAD092TR
14	150.4	15.0	535	7	CR558426 DKFZp459J
15	150.2	15.0	541	7	CR263446 170004240
16	150.1	15.0	338	2	AW023111 df49d08.Y
17	149.8	15.0	453	8	AQ285718 RPCI11-87
18	149.2	14.9	794	1	AI908575 RC-BT177-
19	149.2	14.9	807	5	B0854654 AGENCOURT
20	149.1	14.9	655	8	AQ275774 CITBI-E1-
21	149.0	14.9	868	2	BF337291 602034658
22	148.8	14.9	379	8	AQ083206 RPCI11-54
23	148.8	14.9	631	8	AQ382985 RPCI11-13
24	148.8	14.9	2332	3	CR601647 full-leng

C 25	148.6	14.8	669	9	AG182560	Pan trogl
26	148.4	14.8	7182	3	HSMB08434	EX648286 Homo sapi
27	148.2	14.8	597	8	AQ035555	CIT-HSP-2
28	148.1	14.8	383	1	A584125	nc10G08.5
29	148.0	14.8	444	8	AQ076419	CIT-HSP-2
30	147.8	14.8	700	7	CN412525	170005325
31	147.6	14.7	529	4	BG618537	602645441
32	147.6	14.7	554	4	BG546209	BG546209 602573433
33	147.6	14.7	627	5	BU675707	UI-CF-DU1
34	147.6	14.7	693	9	AG115646	Pan trogl
35	147.6	14.7	851	6	CB958913	AGENCOURT
36	147.6	14.7	930	5	BQ710436	AGENCOURT
37	147.4	14.7	484	8	AQ275681	CITBI-E1-
38	147.4	14.7	787	6	CB310629	AGENCOURT
39	147.2	14.7	489	8	AQ190713	HS 3231 B
40	147.2	14.7	507	7	CN360588	176005325
41	147.2	14.7	576	4	BM709044	UI-E-CQ1-
42	147.2	14.7	585	6	CD710540	EST-7067
43	147.2	14.7	720	8	BZ772985	mcv59H03.
44	147.2	14.7	762	4	BG562992	602581160
45	147.2	14.7	771	4	BG624056	602648246

ALIGNMENTS

RESULT 1
BC047287
LOCUS BC047287 2191 bp mRNA linear HTC 03-MAR-2003
DEFINITION Homo sapiens, purinergic receptor P2X-like 1, orphan receptor,
clone IMAGE:5198937, mRNA.
ACCESSION BC047287
VERSION BC047287.1 GI:28703829
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2191)
Strausberg, R.
Direct Submission
Submitted (28-FEB-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., McGaspri, R.,
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 93 Row: 1 Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4885534
This clone has the following problem: frame shifted.

FEATURES
Location/Qualifiers
1..2191
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP Sub5"
/clone="IMAGE:1519937"
/tissue_type="Brain, adult, 6 pooled whole brains"
/clone_lib="NIH MGC_114"
/lab_host="DH10B"
/notes="vector: pCWV-SPORT6"

ORIGIN
Query Match      15.5%; Score 154.8; DB 3; Length 2191;
Best Local Similarity 71.1%; Pred. No. 1e-19;
Matches 281; Conservative 0; Mismatches 22; Indels 93; Gaps 2;

QY 107 CCAGTCCCAATGCCCTTGAGACCTGGGACCCACCTATTTTAAGCACTGCGGCTATGAAC 166
DB 618 CTAAGTCCCAATGCCCTTGAGACCTGGGACCCACCTATTTTAAGCACTGCGGCTATGAAC 677
QY 167 CACAATTCAGCCCTACTGTCCCGTGTTCGCACTGGGACCTCGTGGCCAAAGCTGGAG 226
DB 678 CACAATTCAGCCCTACTGTCCCGTGTTCGCACTGGGACCTCGTGGCCAAAGCTGGAG 737
QY 227 GGACCTTCAGAGACCTGGGCTGTGTGGTGTCCCAAGTTGGGGCAGGGTTCCTAGAGG 286
DB 738 GGACCTTCAGAGACCTGGGCTGTGTGGTGTCCCAAGTTGGGGCAGGGTTCCTAGAGG 762
QY 287 GCTCTGGGAGAGGGTCCCGGGCCACCCACCCCGGTGGAAAGCTATGTCTATGTGACGGG 346
DB 763 -----GGG 765
QY 347 TGGCTCTGTAGGCATCAGATTCCTGCGATTTGACCTGACACCCGGGACTCTGCTG 406
DB 766 TGGCTCTGTAGGCATCAGATTCCTGCGATTTGACCTGACACCCGGGACTCTGCTG 825
QY 407 CTGGGCTCACTACTCTCTCCAGCTGCAGAGAGAGCTACAACTTCAGGTGAGGC-CCCA 465
DB 826 CTGGGCTCACTACTCTCTCCAGCTGCAGAGAGAGCTACAACTTCAGGTGAGGC-CCCA 885
QY 466 CTGGTCCCAAGTCCCGAGTGTGGGCCCATCGCCCT 501
DB 886 CTGGTGGGAGCAACCGGGTGTGGAGCCCGCACCT 921

RESULT 2
AW451665      353 bp      mRNA      linear      EST 17-FEB-2000
LOCUS      UI-H-B13-aj-f-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
DEFINITION      IMAGE:2736931 3', mRNA sequence.
ACCESSION      AW451665
VERSION      AW451665.1 GI:6992441
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 353)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Oligo-dT track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=No.
Location/Qualifiers
1..353
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="IMAGE:2736931"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub5"
/notes="Vector: p77T3P-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP Sub5
is a subtracted library derived from NCI_CGAP_Sub4. The
NCI_CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI_CGAP_Kid3 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones) 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3573-3582,
3851-3854 (IMAGE Clones)
1414920-1417991, 1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM
3164-3167, 3716-3720, 3733-3735 (IMAGE Clones)
1257096-1258631, 1469064-1470983, 1475592-1476743);
NCI_CGAP_P122 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE Clones) 985608-986759, 1101192-1101959,
1217928-1220615); NCI_CGAP_Co10 pool 1 LLAM 2644-2653,
2871-2872 (IMAGE Clones)
1057416-1061255, 1144584-1145351). (10% of the driver
population), plus a pool of 3,840 arrayed clones from
NCI_CGAP_Sub1 (IMAGE Clones) 2708616-2710535) and
NCI_CGAP_Sub2 (IMAGE Clones) 2710536-2712435) (10% of
the driver population), plus a pool of 11,136 clones from
NCI_CGAP_Sub3 (IMAGE Clones) 2712456-2723591) (10% of the
driver population), plus a pool of 5,472 clones from
NCI_CGAP_Sub4 (IMAGE Clones) 2723592-2728969) (70% of the
driver population). Subtraction was performed as
previously described (Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_TISSUE=chronic lymphocytic leukemia
TAG_LIB=NCI CGAP_CLL1
TAG_SEQ=ATTGC"

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ORIGIN

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Query Match      15.4%; Score 154.4; DB 2; Length 353;
Best Local Similarity 71.1%; Pred. No. 1.5e-19;
Matches 280; Conservative 0; Mismatches 21; Indels 93; Gaps 2;

QY 109 AGTCCCAATGCCCTTGAGACCTGGGACCCACCTATTTTAAGCACTGCGGCTATGAACCA 168
DB 18 AGTCCCAATGCCCTTGAGACCTGGGACCCACCTATTTTAAGCACTGCGGCTATGAACCA 77
QY 169 CAATTGAGCCCTACTGTCCCGTGTTCGCACTGGGACCTCGTGGCCAAAGCTGAGGG 228
DB 78 CAATTGAGCCCTACTGTCCCGTGTTCGCACTGGGACCTCGTGGCCAAAGCTGAGGG 137
QY 229 ACCTTCGAGACCTGCGGCTGTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGC 288
DB 138 ACCTTCGAGACCTGCGGCTGTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGC 160
QY 289 TCTGGGAGAGGGTCCCGGGCCACCCACCGGTGGAAAGCTATGTCTATGTGTCAGGGTG 348
DB 161 -----GGGTG 165
QY 349 GCTCTGAGGCATCAGATTCCTGCGGATTTGACCTGGACACCCGGGACTCTGGCTGCT 408
DB 166 GCTCTGAGGCATCAGATTCCTGCGGATTTGACCTGGACACCCGGGACTCTGGCTGCT 225
QY 409 GGCCTCACTACTCTCTCCAGCTGCAGAGAGAGCTTACAACTTCAGGTGAGGC-CCCCT 467
DB 226 GGCCTCACTACTCTCTCCAGCTGCAGAGAGAGCTTACAACTTCAGGTGAGGC-CCCCT 285
QY 468 GCTCCAGTGCAGCTGTGGGCCCATCGCCT 501
DB 286 GGTGGGAGCAACCGGGTGTGGAGCCCGCACCT 319

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639 CTGGCTCTACTACTCTCTCCAGCTGCAGAGAAGACTACAACTTCAGGACGCCAC 695

Db

RESULT 4
AI703080
LOCUS
DEFINITION
AI703080 292 bp mRNA linear EST 17-DEC-1999
wds1f03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2338013 3',
similar to SW:P2X6_HUMAN O15547 P2X PURINOCEPTOR 6 ;, mRNA
sequence.
AI703080
AI703080.1 GI:4990980
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 292)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 800 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..292
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2338013"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Ronaldo."

FEATURES
source

Query Match 15.2%; Score 152.6; DB 1; Length 292;
Best Local Similarity 72.8%; Pred. No. 3.5e-19;
Matches 257; Conservative 0; Mismatches 4; Indels 92; Gaps 1;

QY 111 GTCCAAATGCCTTGGAGACCTGGGACCCCACTATTTTAAGCACTGCGCGTATGAACACA 170
Db 2 GTCCAAATGCCTTGGAGACCTGGGACCCCACTATTTTAAGCACTGCGCGTATGAACACA 61

QY 171 ATTCAGCCCCCTACTGTCGCGTGTTCGGACTCGGGACCTCGTGGCCCAAGGCTGGAGGGAC 230
Db 62 ATTCAGCCCCCTACTGTCGCGTGTTCGGACTCGGGACCTCGTGGCCCAAGGCTGGAGGGAC 121

QY 231 CTTTCGAGGACCTGGCGTTGCTGCTGGGTCCCAAGTTGGGGGCGAGGGTTCTTAGAGGGCTC 290
Db 122 CTTTCGAGGACCTGGCGTTGCTGCTGGGTCCCAAGTTGGGGGCGAGGGTTCTTAGAGGGCTC 142

QY 291 TGGGAGAGGGTCCCGGGCCCCACCCAGCTGGAAAGCTATGTGCTATGTGACAGGGTGC 350
Db 143 -----GGGTGC 149

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351 TCTGTAGGCATCAGAGTTTCACTGGGATTGTGACCTGGACACCGGGGACTCTGGCTGCTGG 410
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150 TCTGTAGGCATCAGAGTTTCACTGGGATTGTGACCTGGACACCGGGGACTCTGGCTGCTGG 209
|||||
411 CTTCACTACTCTCTCCAGCTGAGAGAGAGCTACAACTTCAGGTGAGGCC 463
|||||
210 CTTCACTACTCTCTCCAGCTGAGAGAGAGCTACAACTTCAGGTGAGGCC 262

RESULT 5
B56395 525 bp DNA linear GSS 20-JUN-1998
LOCUS CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20,
DEFINITION Genomic survey sequence.
ACCESSION B56395
VERSION B56395.1 GI:2610729
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 525)
AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: CIT-HSP-2006M20.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..525
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7039798"
/db_xref="taxon:9606"
/clone="2006M20"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/notes="Vector: paeloBAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN
Query Match 15.2%; Score 152.4; DB 8; Length 525;
Best Local Similarity 72.8%; Pred. No. 3.6e-19;
Matches 211; Conservative 0; Mismatches 76; Indels 3; Gaps 1;

QY 712 TCCACCCCACTCGGTTCTAGTATCTCCCTCCACAGCAATGGGGTTCATTTTACT 771
| | | | |
Db 177 TTCAGTGTCTCTAGTGTCTTAATTTTCTTAATTTTGTGTTTGTCTTTCTTCT 236
| | | | |
QY 772 TTCCTCTTCCCTTCAGCTTTGTTTTTTTTTTTAAAGACAGAACTCATTTCTGTAC 831
| | | | |
Db 237 TTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTCTCATTTCTGTAC 296
| | | | |
QY 832 CCAGCTGAGTGCAGTGGCCGACCTGGGTCACTGTAACTCTGTTCTCTGGGTTCAA 891
| | | | |
Db 297 CTTGGCTGGAGTGCAGTGGCATGATCTGGGTCACTGCAACCTCTGCTCCCGGTTCAA 356
| | | | |
QY 892 CCGATTCTCCCTTCAGCTTCCTGAGTGTAGTGAATTACAGGTGCTCGCCACTACTCCC 951
| | | | |

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357 GCGATTCTCTGCTCAGTCTCTGAGTAGTGGATTACAGGCATGCACCACCGCT 416
|||||
952 ACCTAATTTTATATTTTGGTAGATAGATGGGTTTTTCACAATGTTGGC 1001
|||||
417 GGCTAATTTTGTATTT---TTAGTAGAGATGGGTTTTTCACAATGTTGGC 463
|||||

RESULT 6
BX504814 414 bp mRNA linear EST 04-SEP-2003
LOCUS DKP2p666J05182_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKP2p666J05182.5, mRNA sequence.
ACCESSION BX504814
VERSION BX504814.1 GI:32032215
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 414)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
TITLE EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
Wellenreuther,R., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZp666J05182) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
Location/Qualifiers
1..414
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp666J05182"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/notes="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI;
cDNA-collection"

ORIGIN
Query Match 15.2%; Score 152.2; DB 5; Length 414;
Best Local Similarity 79.2%; Pred. No. 4e-19;
Matches 194; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 757 TGTTCATTTTACTTCCCTTCCTCCCTTCAGCTTTGTTTTTTTTTTTAAAGACAGA 816
| | | | |
Db 328 TTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTC 269
| | | | |
QY 817 ATCTCATTTCTGTACCCAGGTGTGAGTGCAGTGGCCGACCTCGGCTCACTGTAACTCT 876
| | | | |
Db 268 GTCTTGCTCTGTACCCAGGTGTGAGTGCAGTGGCCGATCTCAGCTCACTGCAGCTCC 209
| | | | |
QY 877 GCTTCCTGGTTTCAACCGATTCTCCTCTCAGCTCTCTGAGTGTGAGTGTGAGTGTG 936
| | | | |
Db 208 ACTTCCGGTTTCAACCGATTCTCCTCTCAGCTCTCTGAGTGTGAGTGTGAGTGTG 149
| | | | |
QY 937 CTCGCCACTACTCCAGCTAAATTTTATATTTTGTGTAGATAGATGGGTTTTTCAATG 996
| | | | |
Db 148 CCGGCCACCATACCCAGCTAAATTTTGTATTT---TTAGTAGAGATGGGATTTTCAACATG 92
| | | | |
QY 997 TTGGC 1001

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Db          91 TTGGC 87

RESULT 7
AG059520/c
LOCUS      AG059520      681 bp      DNA      linear      GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-046L20.F, genomic survey sequence.
ACCESSION  AG059520
VERSION     AG059520.1 GI:16610750
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE  1
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library PTB
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 681)
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpses@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT    Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector      : pKS145
R.Site 1    : SacI
R.Site 2    : SacI
FEATURES    Location/Qualifiers
            1..681
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /clone="PTB-046L20.F"
                /sex="male"
                /cell_type="lymphoblast"
                /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match      15.2%; Score 152.2; DB 9; Length 681;
Best Local Similarity 82.2%; Pred. No. 3.8e-19;
Matches 175; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY      788 CAGCTTTGTTTTTTTTTTTAAAGACAGAACTCTCAATCTGTGTCACCCAGCTGGAGTGCAG 847
Db      507 CAATTTTTTTTTTTTTTTTGTAGAGCGGAGTCTCACTCTGTCCACCGCTGGAGTGCAA 448

QY      848 TGGCCGACCTGGCTCACTGAACCTCTGCTTCTGGGTTCAACCGATTCTCTTCCTC 907
Db      447 TGGCAAACTTGGCTCACTGCACACTCTGCTCCAGGTTCAAGGATTTCTCTGCCTC 388

QY      908 AGCTCTCAGTAGTGGGAATACAGGTGCTGCCACTACTCCAGCTAAATTTTATTT 967
Db      387 AGCTCCCGAGTAGCTAGGATTACAGGTGCTGCCACCATGCCAGCTAAATTTTGT 328

QY      968 TTGGTAGATAGATGGGTTTTCACAAATCTGG 1000
Db      327 ATTTTAGTAGATGGGGTCTCACCATGTTGG 295

RESULT 8
BQ231446
LOCUS      BQ231446      954 bp      mRNA      linear      EST 02-MAY-2002

AGENCOURT 7589565 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6067564
5', mRNA sequence.
ACCESSION  BQ231446
VERSION     BQ231446.1 GI:20412846
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 954)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/,
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            plate: LLAM13347 row: e column: 05
            High quality sequence stop: 576.
            Location/Qualifiers
            1..954
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6067564"
                /tissue_type="embryonal carcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_92"
                /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
                Average insert size 2.5 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC Library."
ORIGIN
Query Match      15.1%; Score 151.6; DB 5; Length 954;
Best Local Similarity 81.8%; Pred. No. 4.7e-19;
Matches 175; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY      788 CAGCTTTGTTTTTTTTTTTAAAGACAGAACTCTCAATCTGTGTCACCCAGCTGGAGTGCAG 847
Db      178 CAGACTTTTTTTTTTTTTTTTGTAGACAGAGTTTCACTCTTGCACCCAGCTGGGTACAA 237

QY      848 TGGCCGACCTGGCTCACTGTAACTCTGCTTCTGGGTTCAACCGATTCTCTTCCTC 907
Db      238 TGGTGTGATCTTGGCCCACTGTAACTCTGCTTCTGGGTTCAAGCATTTCTCTGCTC 297

QY      908 AGCTCTCAGTAGTGGGAATACAGGTGCTGCCACTACTCCAGCTAAATTTTATTT 967
Db      298 AGCTCTCAGTAGTGGGATTACAGGTGCTGCCACACACCTGGCTAAATTTTGTATT 357

QY      968 TTGGTAGATAGATGGGTTTTCACAAATCTGGC 1001
Db      358 TTTTAGTAGATGCGGGGTTTCCCATGTTGGC 391

RESULT 9
BQ231446
LOCUS      BQ231446      1150 bp      mRNA      linear      EST 05-MAR-2002
DEFINITION AGENCOURT_6574865 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732451
5', mRNA sequence.
ACCESSION  BQ231446
VERSION     BQ231446.1 GI:19124386
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```


Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuquai, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Insert length: 431 Std Error: 0.00
 Seq primer: -40m13 fwd. Et from Amersham.

FEATURES

Location/Qualifiers
 1. 322
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:997332"
 /sex="male"
 /tissue_type="invasive prostate tumor"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr10"
 /notes="Organ: prostate; Vector: pAMP10; mRNA made from invasive prostate tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."

ORIGIN

Query Match 15.1%; Score 150.8; DB 1; Length 322;
 Best Local Similarity 80.7%; Pred. No. 7.7e-19;
 Matches 176; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
 QY 784 CCTCAGCTTGTGTTTTTTTTTAAAGACAGAAATCTCATTTCTGTCACCCAGGCTGGAGT 843
 Db 67 CCTCTTGCTCAGCCTCTCTTTTTCAGACAGAGTCTGCTGTGTCACCCAGGCTGGAGT 126
 QY 844 GCAGTGGCCGACCTCGGCTCACTGTAAGCTCTGCTCTGCTGGTTCACCGATTCCTTT 903
 Db 127 GCAGTGGCAGATCTCGGCTCACTGCAACCTCTGCTCTGCTGGTTCACCGATTCCTTT 186
 QY 904 CCTCAGCCTCTGAGTAGTGGAAATACAGGTGCTCGCCACTACTCCAGCTAAATTTTA 963
 Db 187 CCTCAGCCTCTGAGTAGTGGAGTACAGGTGCTCGCCACTACTCCAGCTAAATTTTA 246
 QY 964 TATTTTGGTAGATAGATGGTTTTTCAAAATGTGGC 1001
 Db 247 TAGTATTTTAGTAGAGAAAGGGTTTCACCGTGTAGC 284

RESULT 12

BQ005623
 LOCUS
 DEFINITION
 UI-H-ED0-ayr-a-11-0-UI.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
 IMAGE:5842450 3', mRNA sequence.
 ACCESSION
 BQ005623
 EST
 BQ005623.1 GI:19730523
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 664)
 REFERENCE
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 1-242, >SVA#Other 94-380, >ALU (matched complement)
 394-606, >ALU (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1. 664
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5842450"
 /tissue_type="Chondrosarcoma"
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 /clone_lib="NCI_CGAP_ED0"
 /notes="Organ: Left Pubic Bone; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_ED0 is a cDNA library containing the following tissue(s): Chondrosarcoma cell line CSS. The library was constructed according to Bonaldo, Lennon and Soares Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAGGCT.
 TAG_L1SUB=chondrosarcoma
 TAG_L1B=UI-H-ED0
 TAG_SEQ=CGTCAGGCT"

ORIGIN

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 Db 76 CCTCTTGCTCAGCCTCTCTTTTTCAGACAGAGTCTGCTGTGTCACCCAGGCTGGAGT 135
 QY 844 GCAGTGGCCGACCTCGGCTCACTGTAAGCTCTGCTCTGCTGGTTCACCGATTCCTTT 903
 Db 136 GCAGTGGCAGATCTCGGCTCACTGCAACCTCTGCTCTGCTGGTTCACCGATTCCTTT 195
 QY 904 CCTCAGCCTCTGAGTAGTGGAAATACAGGTGCTCGCCACTACTCCAGCTAAATTTTA 963
 Db 196 CCTCAGCCTCTGAGTAGTGGAGTACAGGTGCTCGCCACTACTCCAGCTAAATTTTA 255
 QY 964 TATTTTGGTAGATAGATGGTTTTTCAAAATGTGGC 1001
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RESULT 13

BZ601931/c
 LOCUS
 DEFINITION
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 ACCESSION
 BZ601931
 VERSION
 BZ601931.1 GI:31510393
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 803)
 REFERENCE
 Volik, S., Zhao, S., Chin, K., Brenner, J. H., Herndon, D. R., Tao, Q., Kowbe, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J. W., and Collins, C.
 End-sequence profiling: Sequence-based analysis of aberrant genomes


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/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/tissue_type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone_lib="GRN EB"  
/notes="oligo dt primed, full-length enriched cdna library  
from embryoid body outgrowths derived from hES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."
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ORIGIN

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Best Local Similarity 83.7%; Pred. No. 9.4e-19;  
Matches 170; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
  
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT  
QY 859 CGGCTC ACTGTAA CCGTCT GCTTCT CCGGTT CAACGAT TCTCTT CCTCAG CCGCTC CTGAG 918  
Db 61 CGGCTC ACTGTCA CCGTCT GCTTCT CCGGTT CAAGTAT TCTCTT CCTCAG CCGCTC CTGAG 120  
QY 919 TAGCTG GAATTAC AGTGTG CTGCGC ACTACT CCGAGC TAAATTTT TATATT TTTGTA GATAG 978  
Db 121 TAGCTG GAATTAC AGTGTG CACAC CACCAT GCGCGC TAAATTTT TTTGTA TTTTAG TAG 180  
QY 979 AGATGG GTTTTC ACATGT TGGC 1001  
Db 181 AGACGG GATTTC ACCATG TTGGC 203
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Search completed: November 21, 2004, 17:35:13
Job time : 3212.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 17:43:16 ; Search time 494.874 Seconds
(without alignments)
10930.100 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues
Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:			
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:			
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6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:			
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1001	100.0	16449	10	US-09-820-095-3
2	393	39.3	576	9	Sequence 3, Appli
3	364	36.4	440	9	Sequence 9249, Ap
4	158.2	15.8	174448	13	US-09-864-761-9249
5	155.8	15.6	301692	16	US-10-087-192-148
6	155.8	15.6	310268	17	US-10-428-487-11
7	155.6	15.5	63045	17	US-10-367-094-195
8	155.6	15.5	63824	15	US-10-714-796-76
9	155.6	15.5	63824	15	US-10-282-174-348
10	155.6	15.5	202100	15	US-10-282-174-348
11	154.8	15.5	2693	10	US-09-820-095-1
12	153.8	15.4	14176	9	US-09-764-864-1644

c	13	153.4	15.3	6248	15	US-10-242-355-705	Sequence 705, App
	14	153	15.3	128779	15	US-10-081-327-38	Sequence 38, Appl
	15	152.6	15.2	588	13	US-10-027-632-77218	Sequence 77218, A
	16	152.6	15.2	588	13	US-10-027-632-300376	Sequence 300376, A
	17	152.6	15.2	588	13	US-10-027-632-77218	Sequence 77218, A
	18	152.6	15.2	588	13	US-10-027-632-300376	Sequence 300376, A
	19	152.2	15.2	32221	9	US-09-764-878-377	Sequence 377, App
c	20	152.2	15.2	32221	14	US-10-079-854-377	Sequence 377, App
	21	152	15.2	527	13	US-10-027-632-130193	Sequence 130193, A
	22	152	15.2	527	13	US-10-027-632-130193	Sequence 130193, A
	23	152	15.2	1364	13	US-10-027-632-253464	Sequence 253464, A
	24	152	15.2	1364	13	US-10-027-632-253464	Sequence 253464, A
	25	152	15.2	1364	13	US-10-027-632-253464	Sequence 253464, A
	26	152	15.2	1364	13	US-10-027-632-253465	Sequence 253465, A
	27	151.8	15.2	631	13	US-10-027-632-57903	Sequence 57903, A
	28	151.8	15.2	631	13	US-10-027-632-57903	Sequence 57903, A
	29	151.8	15.2	631	13	US-10-027-632-79939	Sequence 79939, A
	30	151.8	15.2	631	13	US-10-027-632-79939	Sequence 79939, A
	31	151.8	15.2	649	13	US-10-027-632-6071	Sequence 6071, Ap
	32	151.8	15.2	649	13	US-10-027-632-6071	Sequence 6071, Ap
	33	151.8	15.2	32767	15	US-10-004-113-4	Sequence 4, Appl
	34	151.8	15.2	32767	16	US-10-394-948-4	Sequence 4, Appl
	35	151.2	15.1	43009	13	US-10-087-192-1582	Sequence 1582, Ap
	36	151	15.1	32189	9	US-09-764-878-379	Sequence 379, App
	37	151	15.1	32189	14	US-10-079-854-379	Sequence 379, App
	38	150.8	15.1	529	13	US-10-027-632-267212	Sequence 267212, A
	39	150.8	15.1	529	15	US-10-027-632-267212	Sequence 267212, A
	40	150.8	15.1	98546	13	US-10-087-192-1414	Sequence 1414, Ap
	41	150.8	15.1	107543	17	US-10-322-281-706	Sequence 706, App
	42	150.8	15.1	147309	9	US-09-742-312-3	Sequence 3, Appl
	43	150.8	15.1	147309	15	US-10-436-185-3	Sequence 3, Appl
	44	150.8	15.1	201143	16	US-10-240-425-1059	Sequence 1059, Ap
	45	150.6	15.0	113000	15	US-10-376-566-16	Sequence 16, Appl

ALIGNMENTS

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; Sequence 3, Application US/09820095
; Publication No. US20030233668A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001202
; CURRENT APPLICATION NUMBER: US/09/820,095
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 3
; LENGTH: 16449
; TYPE: DNA
; ORGANISM: Human
US-09-820-095-3

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Db	10060	CAGACCTCTGTGCTCCCTACCTCATCTGACCTTTCCCACTCTCCAGGTCCAATGCC	10119		
Qy	121	TTGAGACCTGGGACCCCACTATTTTAAAGCACTGCGGTATGACACCAATTCAGCCCC	180		
Db	10120	TTGAGACCTGGGACCCCACTATTTTAAAGCACTGCGGTATGACACCAATTCAGCCCC	10179		

QY	181	TACTGTCCCGTGTTC	CGCATTTGGGACCT	CTGTGGCCAA	GGCTGGAGGAC	CTTCGAGAC	240
Db	10180	TACTGTCCCGTGTTC	CGCATTTGGGACCT	CTGTGGCCAA	GGCTGGAGGAC	CTTCGAGAC	10239
QY	241	CTGGGTTGCTGGT	CGGTCCTCAAGTT	GGGCGCAGG	TTCTTAGAGG	CTCTGGAGAGGG	300
Db	10240	CTGGGTTGCTGGT	CGGTCCTCAAGTT	GGGCGCAGG	TTCTTAGAGG	CTCTGGAGAGGG	10299
QY	301	TCCCGGGCCAC	CCACCCGTCAG	CCGTCGAA	AGCTATGTCT	ATGTGACAGG	360
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QY	421	CCTTCCAGCTG	CAGGAGAAG	ACTACA	ACTTCAGT	TGAGGCCCA	480
Db	10420	CCTTCCAGCTG	CAGGAGAAG	ACTACA	ACTTCAGT	TGAGGCCCA	10479
QY	481	AGCTGCTGG	CCCCATG	CCCTCTCA	CTGTGGCG	CCAGGACAG	540
Db	10480	AGCTGCTGG	CCCCATG	CCCTCTCA	CTGTGGCG	CCAGGACAG	10539
QY	541	GGCTCTAG	ATATCCA	CTACGTG	TGTCAAAG	GGGGTCCC	600
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QY	601	AACCCACAT	CTCCAGCAC	AGGCTCCG	TCTGCTGCC	CCCAAGTCT	660
Db	10600	AACCCACAT	CTCCAGCAC	AGGCTCCG	TCTGCTGCC	CCCAAGTCT	10659
QY	661	CATCTGTCC	AGGCCCCCT	GCCAGCT	CAGGCTCCT	CAC	720
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QY	721	CTTCGGTCT	CTAGTATCT	CCCTCC	CACAGAA	TGGGGTGTTC	780
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Db	10840	AGTGCAGT	GCGCCG	ACCTCG	GGTCACT	GTAACTCT	10899
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QY	961	TTATATTT	TGGTAG	ATAGAT	TGGGTTTT	TACAAT	1001
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RESULT 2

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RESULTS 2
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; Sequence 9249, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312

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Db 153 CTGGCGTCTCTGGTGGTCCCAAGTTGGGGCAGGGTCTCTAGAGGGCTCTGGGAGAGGG 94
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Qy 361 TCAGAGTTCACTGGGATTTGACCTGGACACCG 393
Db 33 TCAGAGTTCACTGGGATTTGACCTGGACACCG 1
RESULT 3
US-09-864-761-2179/c
; Sequence 2179, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; SEQ ID NO 2179
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; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.7
US-09-864-761-2179
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Best Local Similarity 100.0%; Pred. No. 2.5e-96;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACAGTCACCTTCAGCAAGTTCACACTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCCCC 60
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Qy 61 CAAGACCCCTCTTGTCTCCCTACCTCATCTGACCTTTCCCACTCTCTCCAGGTCCAATGCC 120
Db 304 CAAGACCCCTCTTGTCTCCCTACCTCATCTGACCTTTCCCACTCTCTCCAGGTCCAATGCC 245
Qy 121 TTGAGACCTTGGGACCCACCTATTATTAGACATCTGGCTATGAACACCAATTCAGCCCC 180
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Qy 181 TACTGTCCCGTGTTCGCCATTGGGGACCTCGTGGCCAAAGCTGGAGGACCTTCGAGGAC 240
Db 184 TACTGTCCCGTGTTCGCCATTGGGGACCTCGTGGCCAAAGCTGGAGGACCTTCGAGGAC 125
Qy 241 CTGGCGTTGCTGTGGTGTCCCAAGTTGGGGGACAGGTTCTTAGAGGCTCTGGGAGAGGG 300
Db 124 CTGGCGTTGCTGTGGTGTCCCAAGTTGGGGGACAGGTTCTTAGAGGCTCTGGGAGAGGG 65
Qy 301 TCCCGGGCCACCCACCGGTGGAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 360
Db 64 TCCCGGGCCACCCACCGGTGGAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 5
Qy 361 TCAG 364
Db 4 TCAG 1
RESULT 4
US-10-087-192-148/c
; Sequence 148, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
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; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-148
Query Match 15.8%; Score 158.2; DB 13; Length 174448;
Best Local Similarity 68.8%; Pred. No. 3.3e-35;
Matches 232; Conservative 0; Mismatches 103; Indels 2; Gaps 1;

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 QY 1000 GC 1001
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 Db 44096 GC 44095

RESULT 8
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 ; Sequence 347, Application US/10282174
 ; Publication No. US20030224380A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Becker, Kenneth David
 ; APPLICANT: Velicelebi, Gonul
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Wang, Xin
 ; APPLICANT: Tanzi, Rudolph E.
 ; APPLICANT: Bertram, Lars
 ; APPLICANT: Saunders, Aleister J.
 ; APPLICANT: Mullin, Kristina M.
 ; APPLICANT: Sampson, Andrew Johnson
 ; APPLICANT: Blacker, Deborah Lynne
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
 ; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
 ; FILE REFERENCE: 37481-3308
 ; CURRENT APPLICATION NUMBER: US/10/282,174
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/339,525
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: US 60/338,010
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/336,929
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/338,363
 ; PRIOR FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/337,052
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: US 60/368,919
 ; PRIOR FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 347
 ; LENGTH: 63824
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(14)
 ; OTHER INFORMATION: N is unknown
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (22880)...(22970)
 ; OTHER INFORMATION: N is unknown
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (39442)...(39541)
 ; OTHER INFORMATION: N is unknown
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (53423)...(53522)
 ; OTHER INFORMATION: N is unknown
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 57620,57642
 ; OTHER INFORMATION: N is unknown
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (57652)...(57751)
 ; OTHER INFORMATION: N is unknown
 ;

US-10-282-174-347

Query Match 15.5%; Score 155.6; DB 15; Length 63824;
 Best Local Similarity 80.6%; Pred. No. 1.4e-34;
 Matches 195; Conservative 0; Mismatches 44; Indels 3; Gaps 1;
 QY 760 TTCAATTTTACTTTCCCTTCTCCCTTCAGCTTTGTTTTTTTTTTTAAACAGAAATC 819
 ||||| |
 Db 45333 TTAATAATTACATTTCCATTCCTCCATTTTCTTTTTTTTTTTTTTTTGGACGGAGTC 45274
 ||||| |
 QY 820 TCATTCTGTACCCAGGCTGGAGTGCAGTGGCCCGACCTCGGCTCACTGTAACTCTGCT 879
 ||||| |
 Db 45273 TCATTCTGTACCCAGGTTGGAGTACAGTGGCAACATCTTGGCTCACTGCAACCTCTGCC 45214
 ||||| |
 QY 880 TCCTGGGTTCAACCGATTTCTCTTCCTCAGCTCTCCTGAGTAGCTGGAAATTACAGGTGCTC 939
 ||||| |
 Db 45213 TCCTGGGTTCAAGTGAATTCCTGCTCAGCTCCGAGTAGCTGGGATTATAGTGTGA 45154
 ||||| |
 QY 940 GCCACTACTCCAGCTAAATTTTATATTTGGTAGATAGAGATGGGTTTTCACAATGTTG 999
 ||||| |
 Db 45153 GCCACCACACCCAGCTAAATTTTGTATTT--TTAGTAGAGATGGGTTTCCCATGTTG 45097
 ||||| |
 QY 1000 GC 1001
 ||
 Db 45096 GC 45095

RESULT 9
 US-10-282-174-348/c
 ; Sequence 348, Application US/10282174
 ; Publication No. US20030224380A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Becker, Kenneth David
 ; APPLICANT: Velicelebi, Gonul
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Wang, Xin
 ; APPLICANT: Tanzi, Rudolph E.
 ; APPLICANT: Bertram, Lars
 ; APPLICANT: Saunders, Aleister J.
 ; APPLICANT: Mullin, Kristina M.
 ; APPLICANT: Sampson, Andrew Johnson
 ; APPLICANT: Blacker, Deborah Lynne
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
 ; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
 ; FILE REFERENCE: 37481-3308
 ; CURRENT APPLICATION NUMBER: US/10/282,174
 ; CURRENT FILING DATE: 2002-10-25
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/339,525
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: US 60/338,010
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/336,929
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/338,363
 ; PRIOR FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/337,052
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: US 60/368,919
 ; PRIOR FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 348
 ; LENGTH: 63824
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 300
 ; OTHER INFORMATION: Insertion: CA following nt 299
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 1152,15104,20815,35719,36738,36739,42125,45083,45887,56706,
 ; LOCATION: 56887,58524,62661,63802
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; OTHER INFORMATION: N is any
; FEATURE:
; NAME/KEY: allele
; LOCATION: 14235
; OTHER INFORMATION: Insertion: T following nt 14234
; FEATURE:
; NAME/KEY: allele
; LOCATION: 41015
; OTHER INFORMATION: Insertion: AATT following nt 41014
US-10-282-174-484

Query Match      15.5%; Score 155.6; DB 15; Length 63824;
Best Local Similarity 80.6%; Pred. No. 1.4e-34;
Matches 195; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY      760 TTCAATTTTACATTCCTCCCTTCCTCCCTTCAGCTTTGTTTTTTTTTTTAAAGACAGAAATC 819
Db      45333 TTAATAATTTACATTTCCATTTCCATTTCTTTTTTTTTTTTTTTTTTTTGGACGGAGTC 183240
QY      820 TCATTCGTGCACCCAGGCTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACCTCTGCT 879
Db      45273 TCATTCGTGCACCCAGGCTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACCTCTGCT 879
QY      880 TCCTGGTTTCAACCGAATTCCTCTCCCTCAGCTCTCTGAGTACAGTGGCAACATCTTGCTCACTGCAACCTCTGCC 939
Db      45214 TCATTCGTGCACCCAGGCTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACCTCTGCC 939
QY      940 GGCACACTCTCCAGCTAAATTTTATATTTTGGTAGATAGAGATGGTTTTCACAATGTTG 999
Db      45154 TCCTGGTTTCAACCGAATTCCTCTCCCTCAGCTCTCTGAGTACAGTGGCAACATCTTGCTCACTGCAACCTCTGCC 939
QY      940 GGCACACTCTCCAGCTAAATTTTATATTTTGGTAGATAGAGATGGTTTTCACAATGTTG 999
Db      45153 GGCACACTCTCCAGCTAAATTTTATATTTTGGTAGATAGAGATGGTTTTCACAATGTTG 999
QY      1000 GC 1001
Db      45096 GC 45095

RESULT 10
US-10-282-174-484/c
; Sequence 484, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 202100

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-174-484

Query Match      15.5%; Score 155.6; DB 15; Length 202100;
Best Local Similarity 80.6%; Pred. No. 2e-34;
Matches 195; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY      760 TTCAATTTTACATTCCTCCCTTCCTCCCTTCAGCTTTGTTTTTTTTTTTAAAGACAGAAATC 819
Db      183299 TTAATAATTTACATTTCCATTTCCATTTCTTTTTTTTTTTTTTTTTTTTGGACGGAGTC 183240
QY      820 TCATTCGTGCACCCAGGCTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACCTCTGCT 879
Db      183239 TCATTCGTGCACCCAGGCTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACCTCTGCC 183180
QY      880 TCCTGGTTTCAACCGAATTCCTCTCCCTCAGCTCTCTGAGTACAGTGGCAACATCTTGCTCACTGCAACCTCTGCC 939
Db      183179 TCCTGGTTTCAACCGAATTCCTCTCCCTCAGCTCTCTGAGTACAGTGGCAACATCTTGCTCACTGCAACCTCTGCC 183120
QY      940 GGCACACTCTCCAGCTAAATTTTATATTTTGGTAGATAGAGATGGTTTTCACAATGTTG 999
Db      183119 GGCACACTCTCCAGCTAAATTTTATATTTTGGTAGATAGAGATGGTTTTCACAATGTTG 183063
QY      1000 GC 1001
Db      183062 GC 183061

RESULT 11
US-09-820-095-1
; Sequence 1, Application US/09820095
; Publication No. US20030233668A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001202
; CURRENT APPLICATION NUMBER: US/09/820,095
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Human
US-09-820-095-1

Query Match      15.5%; Score 154.8; DB 10; Length 2693;
Best Local Similarity 71.0%; Pred. No. 9.5e-35;
Matches 281; Conservative 0; Mismatches 22; Indels 93; Gaps 2;

QY      107 CCAGGTCCCAATGCCCTTGGAGACCTGGGACCCCACTATTTTAAAGCACTGCCCGCTATGAAC 166
Db      567 CTAAGTCCCAATGCCCTTGGAGACCTGGGACCCCACTATTTTAAAGCACTGCCCGCTATGAAC 626
QY      167 CACAATTCAGCCCTACTCTCCGCTGTTCCGATTTGGGACCTCTGTCGCAAGGCTGGAG 226
Db      627 CACAATTCAGCCCTACTCTCCGCTGTTCCGATTTGGGACCTCTGTCGCAAGGCTGGAG 686
QY      227 GGACCTTCGAGGACCTGGGCTTGTGTTGTTCCCAAGTTGGGGGACGGTTTCTTAGAGG 286
Db      687 GGACCTTCGAGGACCTGGGCTTGTGTTGTTCCCAAGTTGGGGGACGGTTTCTTAGAGG 711
QY      287 GCTCTGGGAGAGGTTCCCGGGCCCAACCCACCGGTGGAAGCTATGTGCTATGTGCAGGG 346
Db      712 -----GGG 714
QY      347 TGGCTCTGTAGGCATCAGAGTTTCACTGGGATTTGACCTGGACACCGGGGACTCTGGCTG 406
Db      715 TGGCTCTGTAGGCATCAGAGTTTCACTGGGATTTGACCTGGACACCGGGGACTCTGGCTG 774
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QY 407 CTGGCTCACTACTCTCTCCAGCTGCAGGAGAGAGCTACAACTTCAGGTAGGC-CCCA 465
Db 775 CTGGCTCACTACTCTCTCCAGCTGCAGGAGAGAGCTACAACTTCAGGACAGCCACTCA 834
QY 466 CTGCTCCAGTGGCCAGCTGCTGGGCCCATCGCCCT 501
Db 835 CTGGTGGAGACACGGGTGTGGAGGCCCGCACCT 870

RESULT 12
US-09-764-864-1644/c
; Sequence 1644, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1644
; LENGTH: 14176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1644

Query Match 15.4%; Score 153.8; DB 9; Length 14176;
Best Local Similarity 76.7%; Pred. No. 3.1e-34;
Matches 188; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 757 TGTTCATTTTACTTTCCCTCTCCCTTCAGCTTGTGTTTTTTTTTAAAGACAGA 816
Db 10305 TGGGACATCTTAATAGGCCATGATCTCCCTGGGTTTTTTTTTTTGGGACAGA 10246
QY 817 ATCTCATTCGTCAACAGAGCTGGAGTGCAGTGGCCGACCTGGGCTCATCTGAACCTCT 876
Db 10245 GTCTCGCTCTGTCAACAGAGCTGGAGTGCAGTGGTGTATCTCAACTCACTGCAACCTCT 10186
QY 877 GCTTCCTGGTTCAACCGATTCTCTCTCAGCTCCCTGAGTGTGAATACAGGTG 936
Db 10185 GCCTCTGGTTCAACCGATTCTCTCAGCTCCCTGAGTGTGAATACAGGTG 10126
QY 937 CTGCGCACTACTCCCACTAAATTTTATATTTTGGTAGATAGATGGTTTTTCAATG 996
Db 10125 TGTGCCACAGCGCTGGCTAAATTTTTCGATTTTGTAGTACAGAGCTTTTCATCATG 10066
QY 997 TTGGC 1001
Db 10065 TTGGC 10061

RESULT 13
US-10-242-355-705/c
; Sequence 705, Application US/10242355
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC003C1
; CURRENT APPLICATION NUMBER: US/10/242,355
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,897
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 705
; LENGTH: 6248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-355-705

Query Match 15.3%; Score 153.4; DB 15; Length 6248;
Best Local Similarity 78.3%; Pred. No. 3.1e-34;
Matches 184; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 767 TTACTTTCCCTTCTCCCTTCAGCTTGTGTTTTTTTTTAAAGACAGAACTCATCT 826
Db 3739 TTACAGGCGTCCACCCATCTGCTGTTTTTTTTTTTTTTTGGAGGGAATCTCGCTCT 3680
QY 827 GTCAACCCAGGTGGAGTGCAGTGGCCGCGCTCGCTCACTGTAACTCTCTCTCTGGG 886
Db 3679 GTGCGCCAGGTGGAGGCGAGTGGCAATCTCGCTCACTGTAACTCTCGCTCTGGG 3620
QY 887 TTCAACCCATCTCTCTCTCAGCTCTCTGAGTAGCTGGAATACAGGTGCTCGCCACTA 946
Db 3619 TTACAGGCGTCTCTCTCTCAGCTCTCTGAGTAGCTGGAATACAGGTGCTCGCCACTA 3560
QY 947 CTCCAGCTAAATTTTATATTTTGGTAGATAGATGGTTTTTACAAATGTTGGC 1001
Db 3559 CGCTAACTAAATTTTGTGATTTTGTAGACGCGGTTTCCACGCTGTAGC 3505

RESULT 14
US-10-081-327-38
; Sequence 38, Application US/10081327
; Publication No. US20030129602A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/10/081,327
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 06/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 06/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 128779
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-081-327-38

Query Match 15.3%; Score 153; DB 15; Length 128779;
Best Local Similarity 77.2%; Pred. No. 1e-33;
Matches 186; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 759 TTTCAATTTTACTTTCCCTTCTCCCTTCAGCTTGTGTTTTTTTTTAAAGACAGAA 818
Db 94246 TATAAATTAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 94305
QY 819 CTCATTTCTCAACCCAGCTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACTCTGC 878
Db 94306 CTTACTCTGTCAACCCAGCTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACTCTGC 94365

c	28	144	14.4	15788	4	US-09-920-759-13	Sequence 13, Appl
	29	144	14.4	17493	4	US-09-804-471A-3	Sequence 3, Appl
	30	144	14.4	17493	4	US-10-238-709-3	Sequence 3, Appl
c	31	144	14.4	202001	4	US-09-734-674-3	Sequence 3, Appl
c	32	143.8	14.4	75395	4	US-09-584-890-3	Sequence 3, Appl
c	33	143.8	14.4	75395	4	US-10-274-194-3	Sequence 3, Appl
c	34	143.8	14.3	14636	3	US-09-173-914-6	Sequence 6, Appl
c	35	143.4	14.3	118998	4	US-09-791-105B-32	Sequence 32, Appl
c	36	143.4	14.3	169998	4	US-09-676-610B-24	Sequence 24, Appl
c	37	143.4	14.3	197496	4	US-09-877-177A-10	Sequence 10, Appl
c	38	143.4	14.3	197496	4	US-09-879-409-1	Sequence 1, Appl
c	39	143.4	14.3	319608	4	US-09-539-333D-1	Sequence 1, Appl
c	40	143.2	14.3	3001	4	US-09-539-333D-222	Sequence 222, App
c	41	142.8	14.3	31000	4	US-09-966-451-10	Sequence 10, Appl
c	42	142.8	14.3	55298	4	US-09-491-356C-1	Sequence 1, Appl
c	43	142.8	14.3	70000	4	US-09-851-896-3	Sequence 3, Appl
c	44	142.8	14.3	161652	4	US-09-497-855A-40	Sequence 40, Appl
c	45	142.6	14.2	36651	3	US-09-738-894A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-381-681-1
; Sequence 1, Application US/09381681
; Patent No. 6255472
; GENERAL INFORMATION:
; APPLICANT: TAKIMURA, Takashi
; APPLICANT: NAKAMURA, Yusuke
; TITLE OF INVENTION: HUMAN GENES
; FILE REFERENCE: Q55876
; CURRENT APPLICATION NUMBER: US/09/381.681
; EARLIER FILING DATE: 2000-01-10
; EARLIER APPLICATION NUMBER: JPA 9-093044
; EARLIER FILING DATE: 1997-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Human
US-09-381-681-1

Query Match		15.5%	Score 154.8;	DB 3;	Length 1293;
Best Local Similarity		71.0%	Pred. No. 1.4e-32;		
Matches 281;		Conservative	0;	Mismatches 22;	Indels 93; Gaps 2;
QY	107	CCAGGTCCAAATGCCTTGGAGACCTGGGACCTGGGACCCACCTATTTTAAAGCACTGGCGCTATGAAC	166		
DB	605	CTAAGTCCAAATGCCTTGGAGACCTGGGACCTGGGACCCACCTATTTTAAAGCACTGGCGCTATGAAC	664		
QY	167	CACAAATTCAGCCCTACTGTCCCGTGTTCGCATTTGGGACCTGTGGCAAGCTGGAG	226		
DB	665	CACAAATTCAGCCCTACTGTCCCGTGTTCGCATTTGGGACCTGTGGCAAGCTGGAG	724		
QY	227	GGACCTTCGAGGACCTGGCGTGTTCGTGGTCCAAAGTGGGGGACGGTTCCTAGAGG	286		
DB	725	GGACCTTCGAGGACCTGGCGTGTTCGTGGTCCAAAGTGGGGGACGGTTCCTAGAGG	749		
QY	287	GCTCTGGGAGAGGTCCCGGCCCCACCCACCGGTGGAAGAGCTATGTCTATGTGACGGG	346		
DB	750	-----GGG	752		
QY	347	TGGCTCTGTAGGCATCAGATTCACTGGATTGTGACCTGGACACCGGGACTCTGGCTG	406		
DB	753	TGGCTCTGTAGGCATCAGATTCACTGGATTGTGACCTGGACACCGGGACTCTGGCTG	812		
QY	407	CTGGCCCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACAACCTTCAGGTAGGC-CCCA	465		
DB	813	CTGGCCCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACAACCTTCAGGACGACTCA	872		
QY	466	CTGTCCAGTGGCCAGCTCTGGGCCCATCGCCCT	501		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: November 21, 2004, 12:30:45 ; Search time 83.5046 Seconds
(without alignments)
8520.488 Million cell updates/sec

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Perfect score: 1001
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Scoring table: IDENTITY NUC
Gapex 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/1/ina/5B-COMB.seq.*
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4: /cgn2_6/prodata/1/ina/6B-COMB.seq.*
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6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154.8	15.5	1293	US-09-381-681-1	Sequence 1, Appl
2	154.8	15.5	1360	US-09-191-136-30	Sequence 30, Appl
3	154.8	15.5	1697	US-09-381-681-2	Sequence 2, Appl
4	153	15.3	128779	US-09-497-855A-38	Sequence 38, Appl
5	150	15.0	13204	US-09-054-272-49	Sequence 49, Appl
6	149.2	14.9	70000	US-09-851-896-3	Sequence 3, Appl
7	148.6	14.8	36159	US-09-749-588-3	Sequence 3, Appl
8	148.6	14.8	36159	US-10-135-687-3	Sequence 3, Appl
9	148.4	14.8	48763	US-09-916-204-3	Sequence 3, Appl
10	148.4	14.8	48763	US-10-282-048-3	Sequence 3, Appl
11	147	14.7	8453	US-09-167-681-45	Sequence 45, Appl
12	147	14.7	55298	US-09-491-356C-1	Sequence 1, Appl
13	147	14.7	63000	US-09-780-172-18	Sequence 18, Appl
14	146.2	14.6	72604	US-09-268-992-7	Sequence 7, Appl
15	146.2	14.6	72604	US-09-657-474-7	Sequence 7, Appl
16	145.8	14.6	29629	US-09-729-995-3	Sequence 3, Appl
17	145.8	14.6	29629	US-10-135-689-3	Sequence 3, Appl
18	145.6	14.5	866	US-09-257-179-11	Sequence 11, Appl
19	145	14.5	1001	US-09-541-638-629	Sequence 629, App
20	145	14.5	1001	US-10-170-097-629	Sequence 629, App
21	145	14.5	20674	US-09-641-638-651	Sequence 651, App
22	145	14.5	20674	US-10-170-097-651	Sequence 651, App
23	144.4	14.4	1624	US-08-852-807-10	Sequence 10, Appl
24	144.4	14.4	1624	US-08-832-883-68	Sequence 68, Appl
25	144.4	14.4	9837	US-08-832-877-68	Sequence 68, Appl
26	144.4	14.4	13674	US-08-852-807-1	Sequence 1, Appl
27	144.2	14.4	137000	US-10-172-911-11	Sequence 11, Appl

Db 873 CTGGTGGGAGCAACCGGGGTGTGGAGGCCCGCACCT 908

RESULT 2

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US-09-191-136-30
; Sequence 30, Application US/09191136B
; Patent No. 6214581
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding A Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
; TITLE OF INVENTION: And Use Thereof
; FILE REFERENCES: 6293.US.P1
; CURRENT APPLICATION NUMBER: US/09/191,136B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 09/008,526
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 09/008,185
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,298
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,669
; EARLIER FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequencing Primer (polynucleotide)
US-09-191-136-30

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; Patent No. 6255472
; GENERAL INFORMATION:
; APPLICANT: TAKINO, Takashi
; APPLICANT: NAKAMURA, Yusuke
; TITLE OF INVENTION: HUMAN GENES
; FILE REFERENCE: Q55976
; CURRENT APPLICATION NUMBER: US/09/381,681
; CURRENT FILING DATE: 2000-01-10
; EARLIER APPLICATION NUMBER: JPA 9-093044
; EARLIER FILING DATE: 1997-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(1338)
;
US-09-381-681-2

Query Match 15.5%; Score 154.8; DB 3; Length 1697;
Best Local Similarity 71.0%; Pred.No. 1.6e-32;
Matches 281; Conservative 0; Mismatches 22; Indels 93; Gaps 2

Qy 107 CCAGTCCCAATGCCTTGGAGACCTGGGACCCACCTATTTTAGCACTGCCCTATGAAC 166
Db 650 CTAAGTCCAAATGCCCTTGAGACCTGGGACCCACCTATTTTAAAGCACTGCCGCTATGAAC 709

Qy 167 CACAATTCAGCCCCCTACTGTCCGTGTTCCGCATTTGGGACCTCGTGGCCAAGGCTGGAG 226
Db 710 CACAATTCAGCCCCCTACTGTCCGTGTTCCGCATTTGGGACCTCGTGGCCAAGGCTGGAG 769

Qy 227 GGACCTTCGAGGACCTGCGTGTGCTGGTGGGTCCCAAGTTGGGGGGCAGGGTTCCTAGAGG 286
Db 770 GGACCTTCGAGGACCTGCGGTGTCTT----- 794

Qy 287 GCTCTGGGAGAGGGTCCCGGGCCCAACCCACCGGTGAAAAAGCTATGTCTATGTGCAGGG 346
Db 795 -----GGG 797

Qy 347 TGGCTCTGTAGCATCAGAGTTCACTGGGATTTGACCTGGACACCGGGGACTCTGGCTG 406
Db 798 TGGCTCTGTAGGCATCAGAGTTCACTGGGATTTGACCTGGACACCGGGGACTCTGGCTG 857

Qy 407 CTGGGCTCAGTACTCTTCAGCTGTCAGGAGAGAGCTCAACTTCAGGTGAGGC-CCCA 465
Db 858 CTGGGCTCAGTACTCTTCAGCTGTCAGGAGAGAGCTCAACTTCAGGACAGCACTCA 917

Qy 466 CTGCTCCCAAGTCCCAAGCTGCTGGGCCCATCGCCCT 501
Db 918 CTGTGGGAGCAAACGGGTGTGGAGGCCCACTT 953

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RESULT 3

US-09-381-681-2
; Sequence 2, Application US/09381681

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; ORGANISM: Homo sapiens;
US-09-497-855A-38

Query Match      15.3%; Score 153; DB 4; Length 128779;
Best Local Similarity 77.2%; Pred. No. 3.7e-31;
Matches 186; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 759 TTTTCATTTTACTTCCCTTCTCCCTTCAGCTTTGTTTTTTTTTTTAAAGACAGAT 818
Db 94246 TATAAATTATACATTTTAAATTTTTTATTTCTACTTTTTTTTTTTTTTTGGAGACAAGAT 94305

QY 819 CTCATTTCTGTACCCAGGTGGAGTGCAGTGGCCGACCTCGGCTCACTGTAACTCTTGC 878
Db 94306 CTTACTCTGTACCCAGGTGGAGTGCATAGCGGATCTCGGCTCACTGCAACCTCTGC 94365

QY 879 TTCTGGGTTCACCCAGTCTCTCTTCTCAGCTCTCTGAGTCTGAGTGGATTACAGTGT 938
Db 94366 CTCCCGAGTTCAGAGATTCTTTGTGCTCAGCTCCCGAGTACGTGGATTACAGGCACA 94425

QY 939 CGCCTACTCTCCAGCTAATTTTTTATTTTGGTAGATAGAGTGGGTTTTTACAAATGTT 998
Db 94426 TGCCACACGCCCGCAGCTAATTTTTTGTATTTTGGTAGACGAGTTTCACCATGCT 94485

QY 999 G 999
Db 94486 G 94486

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RESULT 5
US-09-054-272-49/c
; Sequence 49, Application US/09054272
; Patent No. 6692909
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George O.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Rozen, Steven G.
; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH198-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-054-272-49

Query Match      15.0%; Score 150; DB 4; Length 13204;
Best Local Similarity 81.3%; Pred. No. 8.5e-31;
Matches 174; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 788 CAGCTTTGTTTTTTTTTTTTTTTAAAGACAGATCTCTCTGTCACCCAGGTGGAGTGCAG 847
Db 7348 CTGCTTTTTTTTTTTTTTTTTTTTGACAGAGATCTTGTCTGTCAACCAGGTGGAGTGTG 7289

QY 848 TGGCCCGACCTCGGCTCACTGTAACTCTGTTCTCTGGGTTCAACCGAATTCCTCTCCTC 907
Db 7288 TGGCACACTCTTGGCTCACTGCAACCTCTGCTCTCTGGGTTCAAGTCAATTCCTCTGCTT 7229

QY 908 AGCTCTCTGAGTACGTGAATTACAGTGTCTCGCCACTACTCCAGCAATTTTATATT 967
Db 7228 AGCTCTCCGAGTAGCTGGAATTACAGGCATCGGTCAACACCCCGGCTAATTTTTTTTGT 7169

QY 968 TTGTTAGATAGATGGGTTTTTTCAAATGTTGGC 1001
Db 7168 ATTTTAGTAGATGGGTTTTTTCACATGTTGGC 7135

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RESULT 6
US-09-851-896-3
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

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Query Match      14.9%; Score 149.2; DB 4; Length 70000;
Best Local Similarity 81.9%; Pred. No. 3.1e-30;
Matches 172; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 792 TTTGTTTTTTTTTTTTTTTAAAGACAGAAATCTCATCTGTCAACCAGGTGGAGTGCAGTGGC 851
Db 36071 TTTTTTTTTTTTTTTTTTGAGACGGAGTCTGCTCTGTGCCCCAGGCTGGAGTGCAGTGGC 36130

QY 852 CCGACCTCGGCTCACTGTAACTCTGTTCTGGGTTCAACCGAATTCCTCTCTCTCAGCC 911
Db 36131 CGGATCTCGGCTCACTGCAAGCTCCGCTCTCCGGGTTCAAGCAATTCCTCTGCTCAGCC 36190

QY 912 TCCTGAGTAGCTGGAATTACAGGTGCTCGCCACTACTCCAGCAATAATTTTATTTTGG 971
Db 36191 TCCCGCGTAGCTGGGACTACAGGCGCCGCCACACACCCCGGCTAATTTTTTTGTGTTTT 36250

QY 972 TAGATAGATGGGTTTTTTCAAATGTTGGC 1001
Db 36251 TTATAGAGACGGGGTTTTCACCATGTTGGC 36280

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RESULT 7
US-09-749-588-3
; Sequence 3, Application US/09749588
; Patent No. 643521
; GENERAL INFORMATION:
; APPLICANT: CHANDRAMOULISWARAN, Ishwar et al

```



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; LENGTH: 48763
; TYPE: DNA
; ORGANISM: Human
US-10-282-048-3

Query Match          14.8%; Score 148.4; DB 4; Length 48763;
Best Local Similarity 73.7%; Pred. No. 4.3e-30;
Matches 202; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 728 TCTAGTATCTCCCTCCACAGCAATGGGGTGTTCATTTTACTTTCCCTTTCTCCCTT 787
Db 16400 TTTAATCACTCCCTAAAGTCTACCTCGTTTTTTTTTTTGGTTTTTTTTTTTTT 16459

QY 788 CAGCTTTGTTTTTTTTTTTATAGACAGATCTCATTCTGCACCCAGGCTGAGTGCAG 847
Db 16460 TTTTHTTTTTTTTTTTTTTTAGGTAGACTTGTCTCTGCACCCAGGCTGAGTGCAG 16519

QY 848 TGGCCGACCTCGGCTCACTTAACCTCTGCTTCTCTGGGTCAACCGATTCTCCTTCCTC 907
Db 16520 TGGTGGGATCTTGGCTCACTGCAACCTCCACCTCTCTGAGTCAAGCAATTTCTCTGCCTC 16579

QY 908 AGCTCTCTGAGTAGCTGGAAATACAGGTCTCGCCACTACTCCAGCTAATTTTATATT 967
Db 16580 AGCTCTCTGAGTAGCTGGGATTATAGTGCCTGCCACACGCTGCTAATTTTGTGA 16639

QY 968 TTGTAGATAGAGATGGGTTTTTCACAATGTGGC 1001
Db 16640 TTTTAG-TAGAGTTGGGGTTTCAACCATGTGGC 16672

RESULT 11
US-09-167-681-45
; Sequence 45, Application US/09167681A
; Patent No. 6265561
; GENERAL INFORMATION:
; APPLICANT: Weinshilboum, M.D., Richard M.
; APPLICANT: Raitogianis, Rebecca B.
; APPLICANT: Wood, Thomas C.
; APPLICANT: Ottensm, Diane M.
; TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
; FILE REFERENCE: 07039/118001
; CURRENT APPLICATION NUMBER: US/09/167,681A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 847
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4361)...(4507)
; NAME/KEY: CDS
; LOCATION: (4612)...(4737)
; NAME/KEY: CDS
; LOCATION: (4827)...(4925)
; NAME/KEY: CDS
; LOCATION: (6322)...(6447)
; NAME/KEY: CDS
; LOCATION: (6543)...(6638)
; NAME/KEY: CDS
; LOCATION: (7137)...(7316)
; NAME/KEY: CDS
; LOCATION: (7439)...(7553)
; US-09-167-681-45

Query Match          14.7%; Score 147; DB 3; Length 8453;
Best Local Similarity 78.2%; Pred. No. 4.6e-30;
Matches 190; Conservative 0; Mismatches 50; Indels 3; Gaps 1;

QY 759 TTTCAATTTTACTTTCCCTTCCTCCCTTCAGCTTTGTTTTTTTTTTTAAAGACAGAA 818
Db 1668 TATCTCTCTGTTCTTCTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1727

; US-09-491-356C-1
; Sequence 1, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 55298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (485)...(485)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (838)...(838)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (16728)...(16728)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22750)...(22750)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22756)...(22756)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (28519)...(28519)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (44804)...(44804)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (45002)...(45002)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (54049)...(54049)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (54226)...(54226)
; OTHER INFORMATION: n is not determined
; US-09-491-356C-1
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Query Match 14.7%; Score 147; DB 4; Length 55298;
Best Local Similarity 81.0%; Pred. No. 1.1e-29;
Matches 171; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 791 CTTTGTGTTTTTTTTTAAAGACAGAACTCTATTCTGTCACCCAGGCTGGAGTCCAGTGG 850
Db 25227 CTTTGTGTTTTTTTTTAAAGACAGAGCTTGTCTGTGCGCCAGGCTGGAGTCCAGTGG 25286
QY 851 CCGACCTCGGCTCACTGTAACCTCTGCTCTGCTGCTTCAACCGATCTCTCTCTCAGC 910
Db 25287 CCGGATCTCGGCTCACTGTAACCTCTGCTCTGCTGCTTCAACCGATCTCTCTCTCAGC 25346
QY 911 CTCCTGAGTAGCTGGAATTAAGAGTCTGCGCACTACTCCAGCTAAATTTTTATATTG 970
Db 25347 CTCCTGAGTAGCTGGAATTAAGAGTCTGCGCACTACTCCAGCTAAATTTTTATATTG 25406
QY 971 GTAGATAGAGTGGTTTTTACAAATGTTGGC 1001
Db 25407 TTTGCTAGACAGAGGTTCCACCATGTTGGC 25437

RESULT 13
US-09-780-172-18/c
; Sequence 18, Application US/09780172
; Patent No. 6607916
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
; FILE REFERENCE: R15-0159
; CURRENT APPLICATION NUMBER: US/09/780,172
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 63000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-172-18

Query Match 14.7%; Score 147; DB 4; Length 63000;
Best Local Similarity 81.6%; Pred. No. 1.2e-29;
Matches 182; Conservative 0; Mismatches 40; Indels 1; Gaps 1;
QY 779 TCTCCCTTCAGCTTTGTTTTTTTTTAAAGACAGAACTCTATTCTGTCCACCCAGCT 838
Db 50904 TTTTCCCAATTTTTTTTTTTTTTTTTTTTGAAGACGAGTCTGCTGTCCACCCAGCT 50845
QY 839 GGAGTGCAGTCCCGACTCGGCTCACTGTAACCTCTGCTTCTGGGTCAACCGATTG 898
Db 50844 GGAGCAGAGTGCAGATCTGGCTCACTGCAACCTCCGCTCCGGGTTCAGCAATTC 50785
QY 899 TCTTCTCTCAGCTCTCAGTAGTCTGGAATTAAGAGTCTGCGCACTACTCCAGCTAAAT 958
Db 50784 TCTTCTCTCAGCTCTCAGTAGTCTGGAATTAAGAGTCTGCGCACTACTCCAGCTAAAT 50725
QY 959 TTTTATTTTGGTAGATAGAGATGGGTTTTCACAAATGTTGGC 1001
Db 50724 TTTTATTTTGGTAGATAGAGATGGGTTTTCACAAATGTTGGC 50683

RESULT 14
US-09-268-992-7/c
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992

; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, or t
US-09-268-992-7

Query Match 14.6%; Score 146.2; DB 3; Length 72604;
Best Local Similarity 83.3%; Pred. No. 2.1e-29;
Matches 179; Conservative 0; Mismatches 33; Indels 3; Gaps 1;
QY 789 AGCTTTGTTTTTTTTTAAAGACAGAACTCTATTCTGTCCACCCAGGCTGGAGTGCAGT 848
Db 57752 AGCTTTGTTTTTTTTTAAAGACAGAACTCTATTCTGTCCACCCAGGCTGGAGTGCAGT 57693
QY 849 GGCCCGACCTCGGCTCACTGTAACCTCTCTTCTGGGTCAACCGATCTCTCTCTCTCA 908
Db 57692 GGTGCGATCTCGGCTCACTGTAACCTCTCTTCTGGGTCAACCGATCTCTCTCTCA 57633
QY 909 GCCTCTGAGTAGCTGGAATTAAGAGTCTGCGCACTACTCCAGCTAAATTTTTATATT 968
Db 57632 GCCTCTGAGTAGCTGGAATTAAGAGTCTGCGCACTACTCCAGCTAAATTTTTATATT 57573
QY 969 ---TGGTAGATAGAGATGGGTTTTCACAAATGTTGG 1000
Db 57572 GTATTTTAAAGATAGAGATGGGTTTTCACAAATGTTGG 57538

RESULT 15
US-09-657-474-7/c
; Sequence 7, Application US/09657474
; Patent No. 6395762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; CURRENT FILING DATE: 2000-09-07
; EARLIER APPLICATION NUMBER: 09/268,992
; EARLIER FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: all n positions

OTHER INFORMATION: n=a, c, g, or t
US-09-657-474-7

Query Match 14.6%; Score 146.2; DB 3; Length 72604;
Best Local Similarity 83.3%; Pred. No. 2.1e-29;
Matches 179; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

QY 789 AGCTTTGTTTTTTTTTTTTTAAGACAGAACTCATCTGTCAACCGAGGCTGGAGTGCACT 848
DB 57752 AGCTTTGTTTTTTTTTTTTTGGAGTGGAGTCTGCTCTCAACCGAGGCTGGAGTGCAAT 57693

QY 849 GGCCCGACCTCGGCTCACTGTAACTCTGCTTCTGGGTTCAACCGAATCTCCTTCCTCA 908
DB 57692 GGTGCGATCTCGGCTCACTGCAACCTCTGCTCTGGGTTCAACAAATCTCTGCTCA 57633

QY 909 GCTCTCTGAGTAGCTGGATTACAGGTGCTGCCACTACTCCAGCTAATTTTATATTT 968
DB 57632 GCTCTCTGAGTAGCTGGGATTACAGGCACGCGCCACCATGACCGAGCTAATATTTTTTT 57573

QY 969 ---TGGTAGATAGATGGGTTTTTCACAATGTTGG 1000
DB 57572 GTATTTTAAATAGATGGGGTTTCACCATGTTGG 57538

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 12:30:45 ; Search time 479.756 Seconds
(without alignments)
10952.804 Million cell updates/sec

Title: US-09-820-095B-3_COPY_10000_11000

Perfect score: 1001
Sequence: 1.acacagtcaccttcagcaag.....tgggttttcacaatgttggc 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
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8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	393	39.3	576	4	AAL43700	AAL43700 Probe #12
4	393	39.3	576	4	ABA30783	ABA30783 Probe #92
5	393	39.3	576	4	AAL12112	AAL12112 Human bra
6	393	39.3	576	4	ABS37461	ABS37461 Human liv
7	393	39.3	576	6	ABS11822	ABS11822 Human gen
8	364	36.4	440	4	AAL12260	AAL12260 Probe #21
9	364	36.4	440	4	ABA53963	ABA53963 Human foe
10	364	36.4	440	4	AAL133615	AAL133615 Probe #23
11	364	36.4	440	4	ABA43513	ABA43513 Human bre
12	364	36.4	440	4	ABA23713	ABA23713 Probe #21
13	364	36.4	440	4	AAK27678	AAK27678 Human don
14	364	36.4	440	4	AAK02232	AAK02232 Human bra
15	364	36.4	440	4	ABS27249	ABS27249 Human liv
16	364	36.4	440	5	AAI02174	AAI02174 Probe #21
17	364	36.4	440	6	ABS02141	ABS02141 Human gen
18	161.2	16.1	9131	12	ADM97830	ADM97830 PXT-CMV-S
19	161.2	16.1	10557	12	ADM97832	ADM97832 PXT-CMV-S
20	157	15.7	7240	4	AAD04467	AAD04467 Human ins
21	157	15.7	7240	4	AAH31267	AAH31267 Human ins

C 22	157	15.7	7240	4	AAL51170	AAL51170 Human ins
C 23	157	15.7	7240	5	AAL50570	AAL50570 Insulin r
C 24	157	15.7	7240	6	ABQ72725	ABQ72725 Human ins
C 25	157	15.7	7240	9	AAL62772	AAL62772 Human ins
C 26	155.6	15.5	63824	10	ADE43742	ADE43742 Human KNS
C 27	155.6	15.5	63824	10	ADE43743	ADE43743 Polymorph
C 28	155.6	15.5	63824	12	ADH54220	ADH54220 Human KNS
C 29	155.6	15.5	63824	12	ADH54221	ADH54221 Human KNS
C 30	155.6	15.5	153170	12	ADQ17382	ADQ17382 Human sof
C 31	155.6	15.5	202100	10	ADE43315	ADE43315 Human IDE
C 32	155.6	15.5	202100	12	ADH54357	ADH54357 Human IDE
C 33	155.2	15.5	471	5	ABV61726	ABV61726 Human pro
C 34	154.8	15.5	1293	2	AAV61832	AAV61832 Coding se
C 35	154.8	15.5	1360	4	AAD04978	AAD04978 Human pur
C 36	154.8	15.5	1452	12	ADP49178	ADP49178 Human P2X
C 37	154.8	15.5	1452	12	ADP49172	ADP49172 Human P2X
C 38	154.8	15.5	1452	12	ADP49182	ADP49182 Human P2X
C 39	154.8	15.5	1452	12	ADP49174	ADP49174 Rat P2X2
C 40	154.8	15.5	1452	12	ADP49176	ADP49176 Human P2X
C 41	154.8	15.5	1697	2	AAV61833	AAV61833 Coding se
C 42	154.8	15.5	2693	8	AAL51048	AAL51048 Human P2X
C 43	153.8	15.4	14176	4	ABS26670	ABS26670 Human gen
C 44	153.8	15.4	14176	8	ABX74019	ABX74019 Human nov
C 45	153.8	15.4	177531	8	ACF62732	ACF62732 Cancer ba

ALIGNMENTS

RESULT 1

AAL51049

ID AAL51049 standard; DNA; 16449 BP.

XX AAL51049;

DT 20-FEB-2003 (first entry)

XX Human P2X-like purinergic receptor G-protein coupled receptor gene.

DE Human; gene; ds; Gene therapy; G-protein coupled receptor; chromosome 22;

XX P2X-like purinergic receptor; anaplastic oligodendroglioma; GPCR;

KW chronic lymphocytic leukaemia; lung carcinoma; colon carcinoma;

KW brain carcinoma; drug screening; tissue typing; pharmacogenomic analysis;

KW SNP; single nucleotide polymorphism.

XX Homo sapiens.

XX Key Location/Qualifiers

PH variation replace(136,C)

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 FT 70472..70661
 FT /tag= lr
 FT /number= 10
 FT 70662..70851
 FT /tag= ls
 FT /number= 10
 FT 70852..71041
 FT /tag= lt
 FT /number= 10
 FT 71042..71231
 FT /tag= lu
 FT /number= 10
 FT 71232..71421
 FT /tag= lv
 FT /number= 10
 FT 71422..71611
 FT /tag= lw
 FT /number= 10
 FT 71612..71801
 FT /tag= lx
 FT /number= 10
 FT 71802..72091
 FT /tag= ly
 FT /number= 10
 FT 72092..72281
 FT /tag

Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ACACAGTCAACCTTCAGCAAGTTCAACTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC	60
Db	10000	ACACAGTCAACCTTCAGCAAGTTCAACTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC	10059
Qy	61	CAAGACCCTCTGTCCCTACCTCATCTGACCTTCCACTCTCTCCAGTGCCTCAATGCC	120
Db	10060	CAAGACCCTCTGTCCCTACCTCATCTGACCTTCCACTCTCTCCAGTGCCTCAATGCC	10119
Qy	121	TTTGAGACCTGGGACCCCACTTATTTTAAGCACCTCCGCTATGAACCAATTCAGCCCC	180
Db	10120	TTTGAGACCTGGGACCCCACTTATTTTAAGCACCTCCGCTATGAACCAATTCAGCCCC	10179
Qy	181	TACTGTCGGTTCGGCAATTTGGGACCTCGTGGCCAAAGCTGGAGGACCTTCGAGGAC	240
Db	10180	TACTGTCGGTTCGGCAATTTGGGACCTCGTGGCCAAAGCTGGAGGACCTTCGAGGAC	10239
Qy	241	CTGGCGTTGCTGGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGGCTCTGGGAGGG	300
Db	10240	CTGGCGTTGCTGGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGGCTCTGGGAGGG	10299
Qy	301	TCCCGGGCCACGCAACGGTGGAAAGCTATGTGCTATGTGCAGGGTGGCTCTGTAGGCA	360
Db	10300	TCCCGGGCCACGCAACGGTGGAAAGCTATGTGCTATGTGCAGGGTGGCTCTGTAGGCA	10359
Qy	361	TCAGAGTTCACTGGGATTGTACCTGGACACCGGGAATCTGGTGTCTGGGCTCACTACT	420
Db	10360	TCAGAGTTCACTGGGATTGTACCTGGACACCGGGAATCTGGTGTCTGGGCTCACTACT	10419
Qy	421	CCTTCAGCTGCAGGAGAGACTACACTTCAGGTGAGGCCCACTGCTCCCACTGCC	480
Db	10420	CCTTCAGCTGCAGGAGAGACTACACTTCAGGTGAGGCCCACTGCTCCCACTGCC	10479
Qy	481	AGTGCTGGGGCCATCGCCCTCTCACTGTGGGGCCAGGACAGACCAACCCAGGCCAG	540
Db	10480	AGTGCTGGGGCCATCGCCCTCTCACTGTGGGGCCAGGACAGACCAACCCAGGCCAG	10539
Qy	541	GCCTCTAGATATTCACACTACGTGTGCAAGGGGTCCCAAGGACGAGAGAGCTGTTCTC	600
Db	10540	GCCTCTAGATATTCACACTACGTGTGCAAGGGGTCCCAAGGACGAGAGAGCTGTTCTC	10599
Qy	601	AACCCACATCTCTCAGCACAGGCTCCGCTCTGCTGCCCAAGTCTTGAGGCCCTCCACC	660
Db	10600	AACCCACATCTCTCAGCACAGGCTCCGCTCTGCTGCCCAAGTCTTGAGGCCCTCCACC	10659
Qy	661	CATCTGTCAGGCCCTCCAGCTCAGGCTCCTCACTGCGAGGCCCTCTCTCCACCCCA	720
Db	10660	CATCTGTCAGGCCCTCCAGCTCAGGCTCCTCACTGCGAGGCCCTCTCTCCACCCCA	10719
Qy	721	CCTCGCTCTAGPATCTCCCTCCACAGCAATGGGGTGTTCATTTTACTTTCCCTCTC	780
Db	10720	CCTCGCTCTAGPATCTCCCTCCACAGCAATGGGGTGTTCATTTTACTTTCCCTCTC	10779
Qy	781	TCCCTCTCAGCTTGTGTTTTTTTTTTTTTTTAAAGACAGATCTCACTCTGTCACCCAGGCTGG	840
Db	10780	TCCCTCTCAGCTTGTGTTTTTTTTTTTTTTTAAAGACAGATCTCACTCTGTCACCCAGGCTGG	10839
Qy	841	AGTGCAATGCCGACCTCGGCTCACTGTAAACCTCTGCTTCTGGGTTCAACCGATCTC	900
Db	10840	AGTGCAATGCCGACCTCGGCTCACTGTAAACCTCTGCTTCTGGGTTCAACCGATCTC	10899
Qy	901	CTTCTCTCAGCTCCTTGAGTAGCTGGAAATACAGGTGCTCGGCACACTCTCCAGCTAAATTT	960
Db	10900	CTTCTCTCAGCTCCTTGAGTAGCTGGAAATACAGGTGCTCGGCACACTCTCCAGCTAAATTT	10959
Qy	961	TTATATTTTGGTAGATAGAGATGGTTTTTCAATGTTGGC	1001
Db	10960	TTATATTTTGGTAGATAGAGATGGTTTTTCAATGTTGGC	11000

RESULT 2
AA118586/C

ID	AAI18586 standard; DNA; 576 BP.	
XX		
AC	AAI18586;	
XX		
DT	12-OCT-2001 (first entry)	
XX		
DE	Probe #8519 for gene expression analysis in human cervical cell sample.	
XX		
KW	Probe; human; microarray; gene expression; cervical epithelial cell;	
KW	cervical cancer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200157278-A2.	
XX		
PD	09-AUG-2001.	
XX		
PF	30-JAN-2001; 2001WC-US000670.	
XX		
PR	04-FEB-2000; 2000US-0180312P.	
PR	26-MAY-2000; 2000US-0207456P.	
PR	30-JUN-2000; 2000US-0060840P.	
PR	03-AUG-2000; 2000US-0063236P.	
PR	21-SEP-2000; 2000US-0234687P.	
PR	27-SEP-2000; 2000US-0236359P.	
PR	04-OCT-2000; 2000GB-00024263.	
XX		
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
XX		
PI	Penn SG, Hanzel DX, Chen W, Rank DR;	
XX		
XX	WPI; 2001-488901/53.	
DR		
XX		
FT	Human genome-derived single exon nucleic acid probes useful for analyzing	
PT	gene expression in human cervical epithelial cells.	
XX		
PS	Claim 25; SEQ ID NO 8519; 487pp; English.	
XX		
CC	The present invention relates to human single exon nucleic acid probes	
CC	(SENPs). The present sequence is one such probe. The SENPs are derived	
CC	from human hela cells. The SENPs can be used to produce a single exon	
CC	microarray, which can be used for measuring human gene expression in a	
CC	sample derived from human cervical epithelial cells. By measuring gene	
CC	expression, the probes are therefore useful in grading and/or staging of	
CC	diseases of the cervix, notably cervical cancer. Note: The sequence data	
CC	for this patent did not form part of the printed specification, but was	
CC	obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pat_sequences	
XX		
SQ	Sequence 576 BP; 123 A; 158 C; 186 G; 109 T; 0 U; 0 Other;	
	Query Match	
	Best Local Similarity 39.3%; Score 393; DB 4; Length 576;	
	Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ACACAGTCACCTTCAGCAAGTTCAACTTCTCTAAGTAAGCAGAGTGGTCTCATCTGCC 60	
DB	393 ACACAGTCACCTTCAGCAAGTTCAACTTCTCTAAGTAAGCAGAGTGGTCTCATCTGCC 334	
QY	61 CAGACCTCTCTGTCCCTACCTCACTGCACCTTCCACTCTCCAGGTCCAATGCC 120	
DB	333 CAGACCTCTCTGTCCCTACCTCACTGCACCTTCCACTCTCCAGGTCCAATGCC 274	
QY	121 TTGAGACCTGGGACCCCACTATTTTAAAGCACTGCGCTATGAACCACAATTGAGCCCC 180	
DB	273 TTGAGACCTGGGACCCCACTATTTTAAAGCACTGCGCTATGAACCACAATTGAGCCCC 214	
QY	181 TACTGTCCCGTGTCCGCATTTGGGACCTCGTGGCCCAAGCTGGAGGACCTTCGAGGAC 240	
DB	213 TACTGTCCCGTGTCCGCATTTGGGACCTCGTGGCCCAAGCTGGAGGACCTTCGAGGAC 154	
QY	241 CTGGCGTGTGTGGTGGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGGCTCTGGAGAGGG 300	

Query Match 39.3%; Score 393; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 5.2e-96;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACAGTCACTTACAGAGTTCAACTTCTTAAGTAAGCAGAGTGGTCTCATCTGCC 60
DB 393 ACACAGTCACTTACAGAGTTCAACTTCTTAAGTAAGCAGAGTGGTCTCATCTGCC 334

QY 61 CAGAGCCCTCTTGTCCCTTACCTCATCTGACCTTTCCCACTCTCCAGGTTCCAATGCC 120
DB 333 CAGAGCCCTCTTGTCCCTTACCTCATCTGACCTTTCCCACTCTCCAGGTTCCAATGCC 274

QY 121 TTGAGACCTGGACCCCACTTATTTAAGCACTGCCGTATCAACCAATTCAGCC 180
DB 273 TTGAGACCTGGACCCCACTTATTTAAGCACTGCCGTATCAACCAATTCAGCC 214

QY 181 TACTGTCCCGTGTTCGCAATTCGGGACCTCGTGGCAAGCTTGGAGGACCTTCGAGGAC 240
DB 213 TACTGTCCCGTGTTCGCAATTCGGGACCTCGTGGCAAGCTTGGAGGACCTTCGAGGAC 154

QY 241 CTGCGCTTGTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGCTCTGGGAGAGG 300
DB 153 CTGCGCTTGTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGCTCTGGGAGAGG 94

QY 301 TCCCGGGCCCACTCGGATTTGACCTGGACACCG 393
DB 33 TCAGAGTTCACTGGGATTGTGACCTGGACACCG 1

RESULT 5
AAK12112/c
ID AAK12112 standard; DNA; 576 BP.
XX AAK12112;
XX
XX
XX 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe SEQ ID NO: 12103.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX

PS Example 4; SEQ ID NO 12103; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 576 BP; 123 A; 158 C; 186 G; 109 T; 0 U; 0 Other;

Query Match 39.3%; Score 393; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 5.2e-96;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACAGTCACTTACAGAGTTCAACTTCTTAAGTAAGCAGAGTGGTCTCATCTGCC 60
DB 393 ACACAGTCACTTACAGAGTTCAACTTCTTAAGTAAGCAGAGTGGTCTCATCTGCC 334

QY 61 CAGAGCCCTCTTGTCCCTTACCTCATCTGACCTTTCCCACTCTCCAGGTTCCAATGCC 120
DB 333 CAGAGCCCTCTTGTCCCTTACCTCATCTGACCTTTCCCACTCTCCAGGTTCCAATGCC 274

QY 121 TTGAGACCTGGGACCCCACTTATTTAAGCACTGCCGTATCAACCAATTCAGCC 180
DB 273 TTGAGACCTGGGACCCCACTTATTTAAGCACTGCCGTATCAACCAATTCAGCC 214

QY 181 TACTGTCCCGTGTTCGCAATTCGGGACCTCGTGGCAAGCTTGGAGGACCTTCGAGGAC 240
DB 213 TACTGTCCCGTGTTCGCAATTCGGGACCTCGTGGCAAGCTTGGAGGACCTTCGAGGAC 154

QY 241 CTGCGCTTGTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGCTCTGGGAGAGG 300
DB 153 CTGCGCTTGTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGCTCTGGGAGAGG 94

QY 301 TCCCGGGCCCACTCGGATTTGACCTGGACACCG 393
DB 93 TCCCGGGCCCACTCGGATTTGACCTGGACACCG 1

QY 361 TCAGAGTTCACTGGGATTGTGACCTGGACACCG 393
DB 33 TCAGAGTTCACTGGGATTGTGACCTGGACACCG 1

RESULT 6
ABS37461/c
ID ABS37461 standard; DNA; 576 BP.
XX ABS37461;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver single exon probe, SEQ ID No 12451.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
XX hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX coronary heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.

```
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
PT Claim 1; SEQ ID NO 12451; 658pp; English.
PS
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 576 BP; 123 A; 158 C; 186 G; 109 T; 0 U; 0 Other;
XX
XX Query Match 39.3%; Score 393; DB 4; Length 576;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-96;
XX Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ACACAGTCACCTTCAGCAAGTTCAACTCTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
DB 393 ACACAGTCACCTTCAGCAAGTTCAACTCTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 334
QY 61 CAAGACCTTCCTGTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 333 CAAGACCTTCCTGTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 274
QY 121 TTGGAGACTGGGACCCCACTTATTTAAGCACTGCCCTATGAACCAATTCAGCCCC 180
DB 273 TTGGAGACTGGGACCCCACTTATTTAAGCACTGCCCTATGAACCAATTCAGCCCC 214
QY 181 TACTCTCCGTGTTCCGCAATTTGGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 213 TACTCTCCGTGTTCCGCAATTTGGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 154
QY 241 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 153 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 94
QY 301 TCCCGGGCCACCCACCGTGGAAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 93 TCCCGGGCCACCCACCGTGGAAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 34
QY 361 TCAGAGTTCACTGGGATTTGACCTGGGACCG 393
DB 33 TCAGAGTTCACTGGGATTTGACCTGGGACCG 1
XX
RESULT 7
ABSI1822/c
ID ABSI1822 standard; DNA; 576 BP.
XX
XX ABSI1822;
XX
XX ABSI1822;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human genome-derived single exon probe from lung SEQ ID No 11813.
XX
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KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
XX Claim 1; SEQ ID NO 11813; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 16614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
```


PT	Human genome-derived single exon nucleic acid probes useful for analyzing	
PT	gene expression in human cervical epithelial cells.	
XX		
XX	claim 25; SEQ ID NO 2193; 487pp; English.	
CC	The present invention relates to human single exon nucleic acid probes	
CC	(SENPs). The present sequence is one such probe. The SENPs are derived	
CC	from human HeLa cells. The SNPs can be used to produce a single exon	
CC	microarray, which can be used for measuring human gene expression in a	
CC	sample derived from human cervical epithelial cells. By measuring gene	
CC	expression, the probes are therefore useful in grading and/or staging of	
CC	diseases of the cervix, notably cervical cancer. Note: The sequence data	
CC	for this patent did not form part of the printed specification, but was	
CC	obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pt_sequences	
XX		
XX	Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;	
XX		
XX	Query Match 36.4%; Score 364; DB 4; Length 440;	
XX	Best Local Similarity 100.0%; Pred. No. 3.3e-88;	
XX	Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ACACAGTCACCTTCAGCAAGTTCACACTTCTCTAAGTAAGCAGAGTGGTCTCATCTGCCC	60
Db	364 ACACAGTCACCTTCAGCAAGTTCACACTTCTCTAAGTAAGCAGAGTGGTCTCATCTGCCC	305
Qy	61 CAAGACCTCTTGTCGCCCTACCTCATCTGACCTTTCCCACTCTCCAGGTCCAATGCC	120
Db	304 CAAGACCTCTTGTCGCCCTACCTCATCTGACCTTTCCCACTCTCCAGGTCCAATGCC	245
Qy	121 TTGGAGACCTGGACCCCACTATTTTAAAGCATCTGCCGTATGAACACAAATTCAGCCCC	180
Db	244 TTGGAGACCTGGACCCCACTATTTTAAAGCATCTGCCGTATGAACACAAATTCAGCCCC	185
Qy	181 TACTGTCCCGTGTTCGCGATTTGGGACCTCTGTCGCCAAGGCTGGAGGACCTTCGAGGAC	240
Db	184 TACTGTCCCGTGTTCGCGATTTGGGACCTCTGTCGCCAAGGCTGGAGGACCTTCGAGGAC	125
Qy	241 CTGGCGTTGCTGTGGGTCCCAAGTTTGGGGCGAGGGTTCCTAGAGGCTCTGGGAGAGGG	300
Db	124 CTGGCGTTGCTGTGGGTCCCAAGTTTGGGGCGAGGGTTCCTAGAGGCTCTGGGAGAGGG	65
Qy	301 TCCGGGGCCCAACCCACCGGTGGAAAGCTATGTCTATGTGCAGGGTGGCTCTGTAGGCA	360
Db	64 TCCCGGGCCCAACCCACCGGTGGAAAGCTATGTCTATGTGCAGGGTGGCTCTGTAGGCA	5
Qy	361 TCAG 364	
Db	4 TCAG 1	
XX		
XX	RESULT 9	
XX	ABA53963/C	
ID	ABA53963 standard; DNA; 440 BP.	
XX		
AC	ABA53963;	
XX		
XX	01-FEB-2002 (first entry)	
XX		
DE	Human foetal liver single exon nucleic acid probe #2268.	
XX		
KW	Human; foetal liver; gene expression; single exon nucleic acid probe; ss.	
OS	Homo sapiens.	
XX		
XX	WO200157277-A2.	
XX		
PD	09-AUG-2001.	
XX		
FF	30-JAN-2001; 2001WO-US0000669.	
XX		
XX	04-FEB-2000; 2000US-0180312P.	
PR	26-MAY-2000; 2000US-0207456P.	
PR		

CC	specification, but was obtained in electronic format directly from WIPO
XX	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 576 BP; 123 A; 158 G; 186 G; 109 T; 0 U; 0 Other;
	Query Match 39.3%; Score 393; DB 6; Length 576;
	Best Local Similarity 100.0%; Pred. No. 5.2e-96;
	Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGCGTCTCATCTGCC 60
DB	393 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGCGTCTCATCTGCC 334
QY	61 CAAGACCTCTGTGCCCCCTACCTCATCTGACCTTCCCACCTCCCTCCAGGTCCTAATGCC 120
DB	333 CAAGACCTCTGTGCCCCCTACCTCATCTGACCTTCCCACCTCCCTCCAGGTCCTAATGCC 274
QY	121 TTGGAGACCTGGGACCCACCCTATTAAAGCACTGCCTATGAACCAACAATTCAGCCCC 180
DB	273 TTGGAGACCTGGGACCCACCCTATTAAAGCACTGCCTATGAACCAACAATTCAGCCCC 214
QY	181 TACTGTCCGTGTTCCGCATTTGGGACCTCTGTCGCAAGCTGAGGTCGAGGACCTTCAGGAC 240
DB	213 TACTGTCCGTGTTCCGCATTTGGGACCTCTGTCGCAAGCTGAGGTCGAGGACCTTCAGGAC 154
QY	241 CTGGCGTTGTTGGTGGTCCCAAGTTGGGGCACGGTTCCTAGAGGCTCTGGGAGAGGG 300
DB	153 CTGGCGTTGTTGGTGGTCCCAAGTTGGGGCACGGTTCCTAGAGGCTCTGGGAGAGGG 94
QY	301 TCCCGGCCCCACCCACCGGTGGAAAAGCTATGTGCTATGTGCAGGTTGGCTCTGTAGGCA 360
DB	93 TCCCGGCCCCACCCACCGGTGGAAAAGCTATGTGCTATGTGCAGGTTGGCTCTGTAGGCA 34
QY	361 TCAGAGTTCACTGGGATTGTGACTGGACACCG 393
DB	33 TCAGAGTTCACTGGGATTGTGACTGGACACCG 1
RESULT 8	
ID	AA112260/c
XX	AA112260 standard; DNA; 440 BP.
AC	AA112260;
XX	
DT	12-OCT-2001 (first entry)
XX	
DE	Probe #2193 for gene expression analysis in human cervical cell sample.
XX	
KW	Probe; human; microarray; gene expression; cervical epithelial cell;
KX	cervical cancer; ss.
OS	Homo sapiens.
XX	
FN	WO200157278-A2.
XX	
PD	09-AUG-2001.
XX	
Pf	30-JAN-2001; 2001WO-US000670.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-0060840B.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-00234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024363.
XX	(MOLE-) MOLECULAR DYNAMICS INC.
PA	
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-488901/53.
XX	

PT	Human genome-derived single exon nucleic acid probes useful for analyzing
XX	gene expression in human cervical epithelial cells.
PS	Claim 25; SEQ ID NO 2193; 487pp; English.
XX	
CC	The present invention relates to human single exon nucleic acid probes
CC	(SENPs). The present sequence is one such probe. The SENPs are derived
CC	from human HeLa cells. The SENPs can be used to produce a single exon
CC	microarray, which can be used for measuring human gene expression in a
CC	sample derived from human cervical epithelial cells. By measuring gene
CC	expression, the probes are therefore useful in grading and/or staging of
CC	diseases of the cervix, notably cervical cancer. Note: The sequence data
CC	for this patent did not form part of the printed specification, but was
CC	obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;
	Query Match 36.4%; Score 364; DB 4; Length 440;
	Best Local Similarity 100.0%; Pred. No. 3.3e-88;
	Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGCGTCTCATCTGCC 60
DB	364 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGCGTCTCATCTGCC 305
QY	61 CAAGACCTCTCTGTGCCCTACCTCATCTGACCTTCCCACCTCCCTCCAGGTCCTAATGCC 120
DB	304 CAAGACCTCTCTGTGCCCTACCTCATCTGACCTTCCCACCTCCCTCCAGGTCCTAATGCC 245
QY	121 TTGGAGACCTGGGACCCACCCTATTAAAGCACTGCCGCTATGAACCAACAATTCAGCCCC 180
DB	244 TTGGAGACCTGGGACCCACCCTATTAAAGCACTGCCGCTATGAACCAACAATTCAGCCCC 185
QY	181 TACTGTCCCGTGTTCGCAATTGGGACCTCTGTCGGCCAAGGCTGGAGGACCTTCGAGGAC 240
DB	184 TACTGTCCCGTGTTCGCAATTGGGACCTCTGTCGGCCAAGGCTGGAGGACCTTCGAGGAC 125
QY	241 CTGGCGTTGCTGTGGTCCCAAGTTGGGGGACGGTTCCTAGAGGCTCTGGGAGAGGG 300
DB	124 CTGGCGTTGCTGTGGTCCCAAGTTGGGGGACGGTTCCTAGAGGCTCTGGGAGAGGG 65
QY	301 TCCCGGGCCCCACCCACCGGTGGAAAAGCTATGTGCTATGTGCAGGTTGGCTCTGTAGGCA 360
DB	64 TCCCGGGCCCCACCCACCGGTGGAAAAGCTATGTGCTATGTGCAGGTTGGCTCTGTAGGCA 5
QY	361 TCAG 364
DB	4 TCAG 1
RESULT 9	
ID	ABA53963/c
XX	ABA53963 standard; DNA; 440 BP.
AC	ABA53963;
XX	
DT	01-FEB-2002 (first entry)
XX	
DE	Human foetal liver single exon nucleic acid probe #2268.
XX	
KW	Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
OS	Homo sapiens.
XX	
FN	WO200157277-A2.
XX	
PD	09-AUG-2001.
XX	
Pf	30-JAN-2001; 2001WO-US000669.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
XX	

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PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX Claim 1; SEQ ID NO 2268; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;
XX
Query Match 36.4%; Score 364; DB 4; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.3e-88;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ACACAGTCACTTCAGCAAGTTCAACTTCTTAAGTAAAGCAGAGTGGGTCTCATCTGCC 60
DB 364 ACACAGTCACTTCAGCAAGTTCAACTTCTTAAGTAAAGCAGAGTGGGTCTCATCTGCC 305
XX
QY 61 CAAGACCTCTTGTCCCTACCTCATCTGACCTTCCACTTCCCTCCAGGTCCAATGCC 120
DB 304 CAAGACCTCTTGTCCCTACCTCATCTGACCTTCCACTTCCCTCCAGGTCCAATGCC 245
XX
QY 121 TTGGAGACTCGGGACCCACCTATTTTAAAGCACTGCCCTATGAACCAATTCAGCCCC 180
DB 244 TTGGAGACTCGGGACCCACCTATTTTAAAGCACTGCCCTATGAACCAATTCAGCCCC 185
XX
QY 181 TACTGTCCGTGTTCCGATTTGGGACCTCTGAGAGGCTTCCTAGAGGCTCTGAGGAC 240
DB 184 TACTGTCCGTGTTCCGATTTGGGACCTCTGAGAGGCTTCCTAGAGGCTCTGAGGAC 125
XX
QY 241 CTGGGCTTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGCTCTGGGAGAGG 300
DB 124 CTGGGCTTGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGCTCTGGGAGAGG 65
XX
QY 301 TCCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGAGGGTGGCTCTGTAGGCA 360
DB 64 TCCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGAGGGTGGCTCTGTAGGCA 5
XX
QY 361 TCAG 364
DB 4 TCAG 1
XX
RESULT 10
ID AA133615/c
XX AA133615 standard; DNA; 440 BP.
XX
AC AA133615;
XX
XX 17-OCT-2001 (first entry)
XX
XX Probe #2301 used to measure gene expression in human placenta sample.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX
XX Genetic disorder; ss.
```

AC ABA43513;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human breast cell single exon nucleic acid probe #2208.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000662.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-496933/54.
 DR
 DR
 XX
 XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX
 XX Claim 1; SEQ ID NO 2208; 327pp + Sequence Listing; English.
 PS
 PS
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a single exon
 CC nucleic acid probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;
 Query Match 36.4%; Score 364; DB 4; Length 440;
 Best Local Similarity 100.0%; Pred. No. 3.3e-88;
 Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACACAGTCACCTTCAGCAAGTTCACCTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
 DB 364 ACACAGTCACCTTCAGCAAGTTCACCTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 305
 QY 61 CAAGACCTCTTGTGCCCTTACTCTACTGACCTTTCCCACTCTCTCCAGGTCCTAATGCC 120
 DB 304 CAAGACCTCTTGTGCCCTTACTCTACTGACCTTTCCCACTCTCTCCAGGTCCTAATGCC 245
 QY 121 TTGGAGACCTGGAGACCCCTTATTTAAGCACTGGCGTATGAACCAATTCAGCCCC 180
 DB 244 TTGGAGACCTGGAGACCCCTTATTTAAGCACTGGCGTATGAACCAATTCAGCCCC 185

QY 181 TACTGTCCCGTGTTCGCAATGGGACCTCGTGCCCAAGGCTGGAGGACCTTCGAGGAC 240
 DB 184 TACTGTCCCGTGTTCGCAATGGGACCTCGTGCCCAAGGCTGGAGGACCTTCGAGGAC 125
 QY 241 CTGCGTGTCTGTGGGTGCCAAGTGGGGCAGGTTCTTAGAGGGCTCTGGGAGAGGG 300
 DB 124 CTGCGTGTCTGTGGGTGCCAAGTGGGGCAGGTTCTTAGAGGGCTCTGGGAGAGGG 65
 QY 301 TCCCGGGCCACCCACCGGTGAAAAAGCTATGTCTATGTGCAGGGTGGCTCTTAGGCA 360
 DB 64 TCCCGGGCCACCCACCGGTGAAAAAGCTATGTCTATGTGCAGGGTGGCTCTTAGGCA 5
 QY 361 TCAG 364
 DB 4 TCAG 1

RESULT 12
 ABA23713/c
 ID ABA23713 standard; DNA; 440 BP.
 XX
 AC ABA23713;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Probe #2179 for gene expression analysis in human heart cell sample.
 XX
 XX Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000666.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-488899/53.
 DR
 DR Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 PT
 XX
 XX Claim 1; SEQ ID NO 2179; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;

Query Match 36.4%; Score 364; DB 4; Length 440;
 Best Local Similarity 100.0%; Pred. No. 3.3e-88;
 Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACAGTCACTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
 DB 364 ACACAGTCACTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 305

QY 61 CAAGACCTCCCTTGTCCCTTACCTCATCTGACCTTTCCCACTCCTCCAGGTCCTCAATGCC 120
 DB 304 CAAGACCTCCCTTGTCCCTTACCTCATCTGACCTTTCCCACTCCTCCAGGTCCTCAATGCC 245

QY 121 TTGGAGACCTGGGACCCCACTTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 180
 DB 244 TTGGAGACCTGGGACCCCACTTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 185

QY 181 TACTGTCCCGTGTTCGCGCATTTGGGACCTTCGTGGCCAAAGCTATGTGTCAGGGTGGCTCTGTAGGCA 360
 DB 64 TCCCGGGCCACCCACCGGTGGAAAGCTATGTGTCAGGGTGGCTCTGTAGGCA 5

QY 361 TCAG 364
 DB 4 TCAG 1

RESULT 13

AAK27678/c
 ID AAK27678 standard; DNA; 440 BP.

XX AAK27678;
 AC
 XX
 DT 06-NOV-2001 (first entry)
 DE Human bone marrow expressed single exon probe SEQ ID NO: 2235.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
 XX Homo sapiens.
 OS
 XX WO200157276-A2.
 PN
 XX
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-488900/53.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX
 XX Example 4; SEQ ID NO 2235; 658pp + Sequence Listing; English.
 PS
 XX

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention.

SQ Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;

Query Match 36.4%; Score 364; DB 4; Length 440;
 Best Local Similarity 100.0%; Pred. No. 3.3e-88;
 Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACAGTCACTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
 DB 364 ACACAGTCACTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 305

QY 61 CAAGACCTCCCTTGTCCCTTACCTCATCTGACCTTTCCCACTCCTCCAGGTCCTCAATGCC 120
 DB 304 CAAGACCTCCCTTGTCCCTTACCTCATCTGACCTTTCCCACTCCTCCAGGTCCTCAATGCC 245

QY 121 TTGGAGACCTGGGACCCCACTTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 180
 DB 244 TTGGAGACCTGGGACCCCACTTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 185

QY 181 TACTGTCCCGTGTTCGCGCATTTGGGACCTTCGTGGCCAAAGCTATGTGTCAGGGTGGCTCTGTAGGCA 360
 DB 64 TCCCGGGCCACCCACCGGTGGAAAGCTATGTGTCAGGGTGGCTCTGTAGGCA 5

QY 361 TCAG 364
 DB 4 TCAG 1

RESULT 14

AAK02232/c
 ID AAK02232 standard; DNA; 440 BP.

XX AAK02232;
 AC
 XX
 DT 05-NOV-2001 (first entry)
 DE Human brain expressed single exon probe SEQ ID NO: 2223.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW ss.
 XX Homo sapiens.
 OS
 XX WO200157275-A2.
 PN
 XX
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001WO-US000667.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA

```
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
DR Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 2223; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
XX Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;
SQ
Query Match 36.4%; Score 364; DB 4; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.3e-88;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACACAGTCACCTTCAGCAAGTTCACACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
Db 364 ACACAGTCACCTTCAGCAAGTTCACACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 305
QY 61 CAAGACCTCTTGTCCCTACCTCATCTGACCTTTCCACCTCTCCCAAGTCCCAATGCC 120
Db 304 CAAGACCTCTTGTCCCTACCTCATCTGACCTTTCCACCTCTCCCAAGTCCCAATGCC 245
QY 121 TTGGAGACCTGGGACCCACCTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 180
Db 244 TTGGAGACCTGGGACCCACCTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 185
QY 181 TACTGTCCGTGTTCGGACCTTCGGACCTTCGGACCTTCGGACCTTCGGAGGAC 240
Db 184 TACTGTCCGTGTTCGGACCTTCGGACCTTCGGACCTTCGGAGGACCTTCGGAGGAC 125
QY 241 CTGGCGCTTCTGGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGGCTCTGGGAGGG 300
Db 124 CTGGCGCTTCTGGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGGCTCTGGGAGGG 65
QY 301 TCCCGGGCCACCCACCGGTGGAAGACTATGTGTATGTGAGGGTGGCTCTGTAGGCA 360
Db 64 TCCCGGGCCACCCACCGGTGGAAGACTATGTGTATGTGAGGGTGGCTCTGTAGGCA 5
QY 361 TCAG 364
Db 4 TCAG 1
RESULT 15
ABS27249/C
ID ABS27249 standard; DNA; 440 BP.
XX
XX ABS27249;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver single exon probe, SEQ ID NO 2239.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
XX Homo sapiens.
OS
XX WO200157273-A2.
PN
XX 09-AUG-2001.
PD
XX
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```
PF 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
XX Claim 1; SEQ ID NO 2239; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENp) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 440 BP; 96 A; 115 C; 143 G; 86 T; 0 U; 0 Other;
SQ
Query Match 36.4%; Score 364; DB 4; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.3e-88;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACACAGTCACCTTCAGCAAGTTCACACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
Db 364 ACACAGTCACCTTCAGCAAGTTCACACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 305
QY 61 CAAGACCTCTTGTCCCTACCTCATCTGACCTTTCCACCTCTCCCAAGTCCCAATGCC 120
Db 304 CAAGACCTCTTGTCCCTACCTCATCTGACCTTTCCACCTCTCCCAAGTCCCAATGCC 245
QY 121 TTGGAGACCTGGGACCCACCTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 180
Db 244 TTGGAGACCTGGGACCCACCTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 185
QY 181 TACTGTCCGTGTTCGGACCTTCGGACCTTCGGACCTTCGGAGGACCTTCGGAGGAC 240
Db 184 TACTGTCCGTGTTCGGACCTTCGGACCTTCGGACCTTCGGAGGACCTTCGGAGGAC 125
QY 241 CTGGCGCTTCTGGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGGCTCTGGGAGGG 300
Db 124 CTGGCGCTTCTGGTGGTCCCAAGTTGGGGCAGGGTTCCTAGAGGGCTCTGGGAGGG 65
QY 301 TCCCGGGCCACCCACCGGTGGAAGACTATGTGTATGTGAGGGTGGCTCTGTAGGCA 360
Db 64 TCCCGGGCCACCCACCGGTGGAAGACTATGTGTATGTGAGGGTGGCTCTGTAGGCA 5
QY 361 TCAG 364
Db 4 TCAG 1
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_btg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_rc.*
11: gb_sts.*
12: gb_sv.*
13: gb_un.*
14: gb_vr.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	990	98.9	147086	9	AC002472 Homo sapi
2	990	98.9	162470	9	AC007664 Homo sapi
3	949.8	94.9	28984	9	AB002059 Homo sapi
4	827.4	82.7	175167	2	AC116044 Papio ham
5	383	39.3	576	6	CQ072719 Sequence
6	393	39.3	576	6	CQ103527 Sequence
7	393	39.3	576	6	CQ177853 Sequence
8	393	39.3	576	6	CQ225612 Sequence
9	393	39.3	576	6	CQ300708 Sequence
10	393	39.3	576	6	CQ338009 Sequence
11	384	36.4	440	6	CQ051345 Sequence
12	384	36.4	440	6	CQ066393 Sequence
13	384	36.4	440	6	CQ093442 Sequence
14	384	36.4	440	6	CQ132213 Sequence
15	364	36.4	440	6	CQ170783 Sequence
16	364	36.4	440	6	CQ199931 Sequence
17	364	36.4	440	6	CQ215400 Sequence
18	364	36.4	440	6	CQ254007 Sequence
19	364	36.4	440	6	CQ291027 Sequence

C	20	364	36.4	440	6	CQ328129 Sequence
	21	229.8	23.0	203973	10	AC115733 Mus muscu
	22	218.8	21.9	164055	2	AC130883 Rattus no
C	23	162.6	16.2	176184	9	AC018845 Homo sapi
	24	162.6	16.2	185281	9	AC007338 Homo sapi
C	25	162	16.2	180750	2	AC097327 Pan trogl
	26	161.2	16.1	127431	9	AC027796 Homo sapi
	27	161.2	16.1	159397	2	AC027040 Homo sapi
C	28	161.2	16.1	200237	9	AF168787 Homo sapi
C	29	158.8	15.9	157069	9	AC010163 Homo sapi
	30	158.8	15.9	161506	9	AL450105 Human DNA
C	31	158.8	15.9	169250	9	AF002812 Homo sapi
	32	158.6	15.8	53645	2	AC084246 Homo sapi
C	33	158.2	15.8	64425	9	AL591368 Human DNA
	34	158.2	15.8	72172	9	AC010311 Homo sapi
	35	158.2	15.8	315681	2	AL353380 Homo sapi
	36	157.8	15.7	147285	2	AC148838 Pan trogl
	37	157.6	15.7	125990	9	AC108734 Homo sapi
	38	157.4	15.7	64923	9	AC002545 Homo sapi
	39	157.4	15.7	65386	2	AC002532 Homo sapi
C	40	157.4	15.7	100634	9	AP001594 Homo sapi
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C	42	157.2	15.7	149320	2	AC126357 Homo sapi
C	43	157.2	15.7	153053	9	AC007533 Homo sapi
C	44	157.2	15.7	182101	9	AC007599 Homo sapi
C	45	157	15.7	7240	6	AX114613 Sequence

ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.
ACCESSION AC002472
VERSION AC002472.8 GI:24137490
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 147086)
AUTHORS Budarf,M.L. and Emanuel,B.S.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 147086)
AUTHORS Zhang,G., Zhan,M., Lao,V. and Roe,B.A.
TITLE Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 147086)
AUTHORS Zhang,G., Lao,V., Zhan,M. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1997) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE 4 (bases 1 to 147086)
AUTHORS Zhang,G., Zhan,M., Budarf,M.L., Emanuel,B.S. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE 5 (bases 1 to 147086)
AUTHORS Zhang,G., Zhan,M., Budarf,M.L., Emanuel,B.S. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE 6 (bases 1 to 147086)
AUTHORS Zhang,G., Zhan,M., Budarf,M.L., Emanuel,B.S. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 7 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (18-NOV-1998) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	ORIGIN	Query Match 98.9%; Score 990; DB 9; Length 147086; Best Local Similarity 99.9%; Pred. No. 5.5e-248; Matches 1001; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 8 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (21-NOV-1998) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Qy 1	ACACAGTCACTTCAGCAAGTTCACAACTTCCTTAAGTAAGCAGAGTGGTCTCATCTGCC 60
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REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 10 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (13-SEP-1999) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Qy 61	CAAGACCTTCCTTGTCCCTTACCTCATCTGACCTTCCACCTCCCTCCAGGTCCTCAATGCC 120
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REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 12 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (19-MAY-2000) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Qy 121	TTGAGACCTTGGGACCCCACTTATTTTAAGCACTGCGCTATGAACCAATTCAGCCCC 180
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REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 16 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (19-MAY-2000) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Qy 241	CTGGCGTCTGCTGGTGGTCCCAAGTTGGGGGAGGCTCTTAGAGGGCTCTGGGAGGG 300
REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 17 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (09-APR-2003) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Db 67554	CTGGCGTCTGCTGGTGGTCCCAAGTTGGGGGAGGCTCTTAGAGGGCTCTGGGAGGG 67613
REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 18 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (19-MAY-2000) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Qy 301	TCCCGGGCCACCCACCGGTGGAAGCTATGTGTATGTGAGGGTGGCTCTGTAGGCA 360
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COMMENT
On Oct 19, 2002 this sequence version replaced gi:22597497.
Because these overlapping clones came from different libraries.

FEATURES
source
1..147086
/organism="Homo sapiens"
/mol_type="genomic DNA"


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RESULT 4
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LOCUS Papio hamadryas clone RP41-7017, *** SEQUENCING IN PROGRESS ***, 11
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ACCESSION AC116044.2 GI:42270667
VERSION HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS Papio hamadryas (hamadryas baboon)
SOURCE Papio hamadryas
ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Papio.
1 (bases 1 to 175167)
Birren, B., Nusbaum, C. and Lander, E.
Papio hamadryas, clone RP41-7017
Unpublished
2 (bases 1 to 175167)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R.,
Landers, T., Lehotzky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., MacDonald, P., Major, J., Marguis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Olivier, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Rette, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. G., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (23-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 175167)

TITLE
JOURNAL
REFERENCE
AUTHORS

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TITLE JOURNAL COMMENT

Direct Submission
Submitted (04-FEB-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 4, 2004 this sequence version replaced gi:19657483.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu

Project Information
Center project name: L12529
Center clone name: 7_O_17

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

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* 6405: gap of 100 bp
* 6505: contig of 5692 bp in length
* 12197: gap of 100 bp
* 12297: contig of 2863 bp in length
* 15159: contig of 100 bp
* 15160: gap of 100 bp
* 15259: contig of 10056 bp in length
* 25316: gap of 100 bp
* 25416: contig of 5398 bp in length
* 79514: gap of 100 bp
* 79514: contig of 10292 bp in length
* 89805: gap of 100 bp
* 89806: contig of 2696 bp in length
* 92602: gap of 100 bp
* 92702: contig of 8471 bp in length
* 101173: gap of 100 bp
* 101273: contig of 13666 bp in length
* 114939: gap of 100 bp
* 115039: contig of 26075 bp in length
* 141114: gap of 100 bp
* 141214: contig of 33954 bp in length.

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FEATURES source

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ORIGIN

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Matches 924;   Conservative 0;   Mismatches 71;   Indels 14;   Gaps 4;

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Qy 181 TACTGTCCGTGTTCGCGCATTTGGGACCTTGGGACCTGCTGGCCACGAGCTCGAGGACCTTCGAGGAC 240

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Db 153868 TACTGTCCGTTTCCGCAATGGGACCTCTGTCGCGAGGCTGGAGGAACTTCGAGAC 153927
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QY 421 CCTTCAGCTGAGGAGAGAGCTACAACTTCAGGTGAGGCGCCCACTGCTCCCACTGCCC 480
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QY 781 TCCCTTCTAGCTTTGTT 832
Db 154467 TCCCTTCTAGCTTTGTT 154526
QY 833 CAGGTGAGTGCAGTGGCGCCAGCTCGCTCACTGTAACCTCTGCTTCTCTGGGTTCAC 892
Db 154527 CAGGTGAGTGCAGTGGCGCCAGCTCGCTCACTGTAACCTCTGCTTCTCTGGGTTCAC 154586
QY 893 CGATTCTCTCTCAGCTCCTGAGTGCAGTGGAAATTCAGGTTGCTCCCACTACTCCCA 952
Db 154587 CGATTCTCTCTCAGCTCCTGAGTGCAGTGGAAATTCAGGTTGCTCCCACTACTCCCA 154645
QY 953 GCTAATTTTATTTTGTAGATAGATGGTTTTTACCAATGTTGC 1001
Db 154646 GCTAATTTTATTTTGTAGATAGATGGTTTTTACCAATGTTGC 154690

RESULT 5
CQ072719/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

CQ072719
Sequence 8519 from Patent WO0157278.
CQ072719
CQ072719.1 GI:41042588
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human hela cells or other human
cervical epithelial cells
Patent: WO 0157278-A 8519 09-AUG-2001;
Aeomica, Inc. (US)

QY 154690 GCTAATTTTATTTTGTAGATAGATGGTTTTTACCAATGTTGC 154690

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source
Location/Qualifiers
1. 576
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN HELA, SIGNAL = 1.4"

ORIGIN
Query Match 39.3%; Score 393; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.6e-92;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACACAGTCACTTCAGCAGTTCACCTCTCTAAGTAAAGCAGAGTGGTCTCATCTGCCCC 60
Db 393 ACACAGTCACTTCAGCAGTTCACCTCTCTAAGTAAAGCAGAGTGGTCTCATCTGCCCC 334
QY 61 CAAGACCTCTCTGTCCTTACCTCATCTGACCTTTCCCACTCTCCAGGTCCAATGCC 120
Db 333 CAAGACCTCTCTGTCCTTACCTCATCTGACCTTTCCCACTCTCCAGGTCCAATGCC 274
QY 121 TTGGAGACTTGGGACCCCACTATTTTAAAGCACTGCGCTATGAACCAATTCAGCCCC 180
Db 273 TTGGAGACTTGGGACCCCACTATTTTAAAGCACTGCGCTATGAACCAATTCAGCCCC 214
QY 181 TACTGTCCCGTGTTCGCGATTGGGACCTCTGCGCAAGGCTGGAGGACCTTCGAGGAC 240
Db 213 TACTGTCCCGTGTTCGCGATTGGGACCTCTGCGCAAGGCTGGAGGACCTTCGAGGAC 154
QY 241 CTGGCGTTCTGCTGGTGGTCCCAAGTTGGGGCAGGGTCTTAGAGGGCTCTGGAGAGGG 300
Db 153 CTGGCGTTCTGCTGGTGGTCCCAAGTTGGGGCAGGGTCTTAGAGGGCTCTGGAGAGGG 94
QY 301 TCCCGGGCCACCCACCGTGGAAAGCTATGCTATGTCAGAGGTGGCTCTGTAGGCA 360
Db 93 TCCCGGGCCACCCACCGTGGAAAGCTATGCTATGTCAGAGGTGGCTCTGTAGGCA 34
QY 361 TCAGAGTTCACCTGGGATTTGACCTGGACACCG 393
Db 33 TCAGAGTTCACCTGGGATTTGACCTGGACACCG 1

RESULT 6
CQ103527/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

CQ103527
Sequence 12386 from Patent WO0157272.
CQ103527
CQ103527.1 GI:41072578
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 12386 09-AUG-2001;
Aeomica, Inc. (US)

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Location/Qualifiers
1. 576
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Best Local Similarity 100.0%; Pred. No. 6.6e-92;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 393 ACACAGTCACCTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 334
Qy 61 CAGAGCCCTCTGTGCTCCCTACTCTATCTGACCTTTCACCTTCCCAAGTCCCAATGCC 120
Db 333 CAGACCCCTCTGTGCTCCCTACTCTATCTGACCTTTCACCTTCCCAAGTCCCAATGCC 274
Qy 121 TTGGAGACCTTGGGACCCCACTTATTTTAAGCACTGCCGTATGAACCAATTCAGCCCC 180
Db 273 TTGGAGACCTTGGGACCCCACTTATTTTAAGCACTGCCGTATGAACCAATTCAGCCCC 214
Qy 181 TACTGTCCCGTGTTCGGCATTTGGGACCTTCGTGGCCAAAGCTGAGGAGGACCTTCGAGGAC 240
Db 213 TACTGTCCCGTGTTCGGCATTTGGGACCTTCGTGGCCAAAGCTGAGGAGGACCTTCGAGGAC 154
Qy 241 CTGGCGTTCCTGTGGGTCCCAAGTTGGGGGAGGTTCTTCTAGAGGGTCTCTGTAGGCA 300
Db 153 CTGGCGTTCCTGTGGGTCCCAAGTTGGGGGAGGTTCTTCTAGAGGGTCTCTGTAGGCA 94
Qy 301 TCCCGGGCCACCCACCGGTGAAAAGCTATGTGCTATGTGACGGTGGGTCTGTAGGCA 360
Db 93 TCCCGGGCCACCCACCGGTGAAAAGCTATGTGCTATGTGACGGTGGGTCTGTAGGCA 34
Qy 361 TCAGAGTTCACCTGGGATTCTGACCTGGACACCG 393
Db 33 TCAGAGTTCACCTGGGATTCTGACCTGGACACCG 1
RESULT 7
LOCUS CQ177853/c 576 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9249 from Patent WO0157274.
ACCESSION CQ177853
VERSION CQ177853.1 GI:41172592
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 9249 09-AUG-2001;
FEATURES
source location/Qualifiers
1. .576
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN HEART, SIGNAL = 4.1"
ORIGIN
Query Match 39.3%; Score 393; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.6e-92;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACAGTCACCTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
Db 393 ACACAGTCACCTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 334
Qy 61 CAGAGCCCTCTGTGCTCCCTACTCTATCTGACCTTTCACCTTCCCAAGTCCCAATGCC 120
Db 333 CAGAGCCCTCTGTGCTCCCTACTCTATCTGACCTTTCACCTTCCCAAGTCCCAATGCC 274
Qy 121 TTGGAGACCTTGGGACCCCACTTATTTTAAGCACTGCCGTATGAACCAATTCAGCCCC 180
Db 273 TTGGAGACCTTGGGACCCCACTTATTTTAAGCACTGCCGTATGAACCAATTCAGCCCC 214
Qy 181 TACTGTCCCGTGTTCGGCATTTGGGACCTTCGTGGCCAAAGCTGAGGAGGACCTTCGAGGAC 240
Db 213 TACTGTCCCGTGTTCGGCATTTGGGACCTTCGTGGCCAAAGCTGAGGAGGACCTTCGAGGAC 154
Qy 241 CTGGCGTTCCTGTGGGTCCCAAGTTGGGGGAGGTTCTTCTAGAGGGTCTCTGTAGGCA 300
Db 153 CTGGCGTTCCTGTGGGTCCCAAGTTGGGGGAGGTTCTTCTAGAGGGTCTCTGTAGGCA 94

Db 153 CTGGCGTTCCTGTGGGTCCCAAGTTGGGGGAGGTTCTTCTAGAGGGTCTCTGTAGGCA 94
Qy 301 TCCCGGGCCACCCACCGGTGAAAAGCTATGTGCTATGTGACGGTGGGTCTGTAGGCA 360
Db 93 TCCCGGGCCACCCACCGGTGAAAAGCTATGTGCTATGTGACGGTGGGTCTGTAGGCA 34
Qy 361 TCAGAGTTCACCTGGGATTCTGACCTGGACACCG 393
Db 33 TCAGAGTTCACCTGGGATTCTGACCTGGACACCG 1
RESULT 8
LOCUS CQ225612/c 576 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 12451 from Patent WO0157273.
ACCESSION CQ225612
VERSION CQ225612.1 GI:41208499
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24283.6<151> 03 October 2000 (03.10.00)<150> US 60/234,687<151> 21 September 2000 (27.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
JOURNAL Molecular Dynamics Sequence Listing Engine
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1. .576
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN ADULT LIVER, SIGNAL = 1.9"
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Query Match 39.3%; Score 393; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.6e-92;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACAGTCACCTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
Db 393 ACACAGTCACCTTTCAGCAAGTTCAACTTCTTAAGTAAGCAGAGTGGGTCTCATCTGCC 334
Qy 61 CAGAGCCCTCTGTGCTCCCTACTCTATCTGACCTTTCACCTTCCCAAGTCCCAATGCC 120
Db 333 CAGAGCCCTCTGTGCTCCCTACTCTATCTGACCTTTCACCTTCCCAAGTCCCAATGCC 274
Qy 121 TTGGAGACCTTGGGACCCCACTTATTTTAAGCACTGCCGTATGAACCAATTCAGCCCC 180
Db 273 TTGGAGACCTTGGGACCCCACTTATTTTAAGCACTGCCGTATGAACCAATTCAGCCCC 214
Qy 181 TACTGTCCCGTGTTCGGCATTTGGGACCTTCGTGGCCAAAGCTGAGGAGGACCTTCGAGGAC 240
Db 213 TACTGTCCCGTGTTCGGCATTTGGGACCTTCGTGGCCAAAGCTGAGGAGGACCTTCGAGGAC 154
Qy 241 CTGGCGTTCCTGTGGGTCCCAAGTTGGGGGAGGTTCTTCTAGAGGGTCTCTGTAGGCA 300
Db 153 CTGGCGTTCCTGTGGGTCCCAAGTTGGGGGAGGTTCTTCTAGAGGGTCTCTGTAGGCA 94
Qy 301 TCCCGGGCCACCCACCGGTGAAAAGCTATGTGCTATGTGACGGTGGGTCTGTAGGCA 360
Db 93 TCCCGGGCCACCCACCGGTGAAAAGCTATGTGCTATGTGACGGTGGGTCTGTAGGCA 34

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QY 361 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 393
Db 33 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 1

RESULT 9
LOCUS CQ300708 576 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11813 from Patent WO0186003.
ACCESSION CQ300708
VERSION CQ300708.1 GI:41261285
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 11813 15-NOV-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..576
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN LUNG, SIGNAL = 1.5"

ORIGIN
Query Match 39.3%; Score 393; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.6e-92;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACAGTCACCTTCAGCAAGTTCACCTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
Db 393 ACACAGTCACCTTCAGCAAGTTCACCTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC 334

QY 61 CAAGACCTCTCTGTCCCTACCTCATCTGACCTTCCACCTCCCTCCAGGTCCTCAATGCC 120
Db 333 CAAGACCTCTCTGTCCCTACCTCATCTGACCTTCCACCTCCCTCCAGGTCCTCAATGCC 274

QY 121 TTGGAGACCTGGAGACCCACCTATTTTAAAGCACTCCGCTATGAACCAATTCAGCCCC 180
Db 273 TTGGAGACCTGGAGACCCACCTATTTTAAAGCACTCCGCTATGAACCAATTCAGCCCC 214

QY 181 TACTGTCCGCTGTTCCGATTCGGGACCTCTGTCGCAAGGCTTGGAGGACCTTCGAGGAC 240
Db 213 TACTGTCCGCTGTTCCGATTCGGGACCTCTGTCGCAAGGCTTGGAGGACCTTCGAGGAC 154

QY 241 CTGGCGTTCCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGCTCTGGGAGAGG 300
Db 153 CTGGCGTTCCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGCTCTGGGAGAGG 94

QY 301 TCCCGGGCCACCCACCGTGGAAAGCTATGTGCTATGTGACGGGTGGCTCTGTAGGCA 360
Db 93 TCCCGGGCCACCCACCGTGGAAAGCTATGTGCTATGTGACGGGTGGCTCTGTAGGCA 34

QY 361 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 393
Db 33 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 1

RESULT 11
LOCUS CQ051345/c 440 bp DNA linear PAT 19-JAN-2004
DEFINITION Sequence 2165 from Patent WO0157270.
ACCESSION CQ051345
VERSION CQ051345.1 GI:41025851
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and hbl 100 cells
JOURNAL Patent: WO 0157270-A 2165 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..440
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN HBL100, SIGNAL = 5"

ORIGIN
Query Match 39.3%; Score 393; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.6e-92;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACAGTCACCTTCAGCAAGTTCACCTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
Db 393 ACACAGTCACCTTCAGCAAGTTCACCTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC 334

QY 61 CAAGACCTCTCTGTCCCTACCTCATCTGACCTTCCACCTCCCTCCAGGTCCTCAATGCC 120
Db 333 CAAGACCTCTCTGTCCCTACCTCATCTGACCTTCCACCTCCCTCCAGGTCCTCAATGCC 274

QY 121 TTGGAGACCTGGAGACCCACCTATTTTAAAGCACTCCGCTATGAACCAATTCAGCCCC 180
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QY 181 TACTGTCCGCTGTTCCGATTCGGGACCTCTGTCGCAAGGCTTGGAGGACCTTCGAGGAC 240
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QY 241 CTGGCGTTCCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGCTCTGGGAGAGG 300
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QY 301 TCCCGGGCCACCCACCGTGGAAAGCTATGTGCTATGTGACGGGTGGCTCTGTAGGCA 360
Db 93 TCCCGGGCCACCCACCGTGGAAAGCTATGTGCTATGTGACGGGTGGCTCTGTAGGCA 34

QY 361 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 393
Db 33 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 1

RESULT 10
LOCUS CQ338009/c 576 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 12103 from Patent WO0157275.
ACCESSION CQ338009
VERSION CQ338009.1 GI:41287080
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and hbl 100 cells
JOURNAL Patent: WO 0157270-A 2165 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..440
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/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN HBL100, SIGNAL = 5"

ORIGIN
Query Match 39.3%; Score 393; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.6e-92;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACAGTCACCTTCAGCAAGTTCACCTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC 60
Db 393 ACACAGTCACCTTCAGCAAGTTCACCTTCTCTAAGTAAGCAGAGTGGGTCTCATCTGCC 334

QY 61 CAAGACCTCTCTGTCCCTACCTCATCTGACCTTCCACCTCCCTCCAGGTCCTCAATGCC 120
Db 333 CAAGACCTCTCTGTCCCTACCTCATCTGACCTTCCACCTCCCTCCAGGTCCTCAATGCC 274

QY 121 TTGGAGACCTGGAGACCCACCTATTTTAAAGCACTCCGCTATGAACCAATTCAGCCCC 180
Db 273 TTGGAGACCTGGAGACCCACCTATTTTAAAGCACTCCGCTATGAACCAATTCAGCCCC 214

QY 181 TACTGTCCGCTGTTCCGATTCGGGACCTCTGTCGCAAGGCTTGGAGGACCTTCGAGGAC 240
Db 213 TACTGTCCGCTGTTCCGATTCGGGACCTCTGTCGCAAGGCTTGGAGGACCTTCGAGGAC 154

QY 241 CTGGCGTTCCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGCTCTGGGAGAGG 300
Db 153 CTGGCGTTCCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGCTCTGGGAGAGG 94

QY 301 TCCCGGGCCACCCACCGTGGAAAGCTATGTGCTATGTGACGGGTGGCTCTGTAGGCA 360
Db 93 TCCCGGGCCACCCACCGTGGAAAGCTATGTGCTATGTGACGGGTGGCTCTGTAGGCA 34

QY 361 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 393
Db 33 TCAGAGTTCACCTGGGATTGTGACCTGGACACCG 1
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Query Match 36.4%; Score 364; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.5e-84;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGACAGAGTGGTCTCATCTGCC 60
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Qy 61 CAGACCTTCCTGTCCCTACTCATCTGACCTTTCCCACTCTCCAGGTCCCAATGCC 120
Db 304 CAGACCTTCCTGTCCCTACTCATCTGACCTTTCCCACTCTCCAGGTCCCAATGCC 245

Qy 121 TTGGAGACCTGGGACCCACCTATTTTAAAGCACTGCCGTATGAACCAATTCAGCCCC 180
Db 244 TTGGAGACCTGGGACCCACCTATTTTAAAGCACTGCCGTATGAACCAATTCAGCCCC 185

Qy 181 TACTGTCCCGTGTTCGGCAATGGGACCTCGTGGCCAAAGCTGGAGGACCTTCAGGAC 240
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Qy 241 CTGGCGTTGCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGTCTGGGAGAGG 300
Db 124 CTGGCGTTGCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGTCTGGGAGAGG 65

Qy 301 TCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 360
Db 64 TCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 5

Qy 361 TCAG 364
Db 4 TCAG 1

RESULT 12
CQ066393/c
LOCUS 440 bp DNA linear PAT 20-JAN-2004
DEFINITION Sequence 2193 from Patent WO0157278.
ACCESSION CQ066393
VERSION CQ066393.1 GI:41036262
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human hela cells or other human
JOURNAL cervical epithelial cells
Patent: WO 0157278-A 2193 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..440
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN HELA, SIGNAL = 4.9"

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Query Match 36.4%; Score 364; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.5e-84;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGACAGAGTGGTCTCATCTGCC 60
Db 364 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGACAGAGTGGTCTCATCTGCC 305

Qy 61 CAGACCTTCCTGTCCCTACTCATCTGACCTTTCCCACTCTCCAGGTCCCAATGCC 120
Db 304 CAGACCTTCCTGTCCCTACTCATCTGACCTTTCCCACTCTCCAGGTCCCAATGCC 245

Qy 121 TTGGAGACCTGGGACCCACCTATTTTAAAGCACTGCCGTATGAACCAATTCAGCCCC 180

Db 244 TTGGAGACCTGGGACCCACCTATTTTAAAGCACTGCCGTATGAACCAATTCAGCCCC 185

Qy 181 TACTGTCCCGTGTTCGGCAATGGGACCTCGTGGCCAAAGCTGGAGGACCTTCAGGAC 240

Db 184 TACTGTCCCGTGTTCGGCAATGGGACCTCGTGGCCAAAGCTGGAGGACCTTCAGGAC 125

Qy 241 CTGGCGTTGCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGTCTGGGAGAGG 300

Db 124 CTGGCGTTGCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGTCTGGGAGAGG 65

Qy 301 TCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 360

Db 64 TCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 5

Qy 361 TCAG 364
Db 4 TCAG 1

RESULT 13
CQ093442/c
LOCUS 440 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 2301 from Patent WO0157272.
ACCESSION CQ093442
VERSION CQ093442.1 GI:41062468
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 2301 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..440
/organism="Homo sapiens"
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/note="MAP TO AC002472.3-EXPRESSED IN PLACENTA, SIGNAL = 6"

ORIGIN

Query Match 36.4%; Score 364; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.5e-84;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTAAGACAGAGTGGTCTCATCTGCC 60
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Qy 61 CAGACCTTCCTGTCCCTACTCATCTGACCTTTCCCACTCTCCAGGTCCCAATGCC 120

Db 304 CAGACCTTCCTGTCCCTACTCATCTGACCTTTCCCACTCTCCAGGTCCCAATGCC 245

Qy 121 TTGGAGACCTGGGACCCACCTATTTTAAAGCACTGCCGTATGAACCAATTCAGCCCC 180

Db 244 TTGGAGACCTGGGACCCACCTATTTTAAAGCACTGCCGTATGAACCAATTCAGCCCC 185

Qy 181 TACTGTCCCGTGTTCGGCAATGGGACCTCGTGGCCAAAGCTGGAGGACCTTCAGGAC 240

Db 184 TACTGTCCCGTGTTCGGCAATGGGACCTCGTGGCCAAAGCTGGAGGACCTTCAGGAC 125

Qy 241 CTGGCGTTGCTGGTGGTCCCAAGTTGGGGCAGAGTTCCTAGAGGGTCTGGGAGAGG 300

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Qy 301 TCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 360

Db 64 TCCGGGCCACCCACCGGTGAAAAGCTATGTCTATGTGACAGGTGGTCTGTAGGCA 5

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QY 361 TCAG 364
Db 4 TCAG 1

RESULT 14
CQ132213/c
LOCUS 440 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 2235 from Patent WO0157276.
ACCESSION CQ132213
VERSION CQ132213.1 GI:41089569
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 2235 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source 1..440
/organism="Homo sapiens"
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Db 124 CTGGCGTTGCTGGTGGTCCCAAGTTGGGGGCAAGGTTCTTAGAGGCTCTGGGAGAGGG 65
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Db 64 TCCCGGGCCACCCACCGGTGGAAGCTATGTCTATGTGCAGGTTGGCTCTGTAGGCA 5
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Db 4 TCAG 1

Search completed: November 22, 2004, 01:15:08
Job time : 4288.34 secs

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DEFINITION Sequence 2179 from Patent WO0157274.
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VERSION CQ170783.1 GI:41165519
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 2235 09-AUG-2001;
Aeomica, Inc. (US)
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Db 4 TCAG 1

RESULT 15
CQ170783/c
LOCUS 440 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 2179 from Patent WO0157274.
ACCESSION CQ170783
VERSION CQ170783.1 GI:41165519
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 2179 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
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/db_xref="taxon:9606"
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Db 64 TCCCGGGCCACCCACCGGTGGAAGCTATGTCTATGTGCAGGTTGGCTCTGTAGGCA 5
QY 361 TCAG 364
Db 4 TCAG 1
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OM protein - protein search, using sw model

Run on: November 21, 2004, 14:42:41 ; Search time 191 Seconds
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2203	99.0	441	2 CAG30421	CAG30421 homo sapi
4	1599	71.8	379	1 P2X6 MOUSE	O54803 mus musculu
5	1554	69.8	379	1 P2X6 RAT	P51579 rattus norv
6	946	42.5	402	2 Q9W80	Q9W80 gallus gall
7	943	42.4	402	2 Q9TAD2	Q9TAD2 gallus gall
8	900.5	40.5	409	2 Q9XK65	Q9XK65 rana catesb
9	892	40.1	455	1 P2X5 RAT	P51578 rattus norv
10	888	39.9	455	2 Q91VE2	Q91VE2 mus musculu
11	885.5	39.8	481	2 Q8JFP7	Q8JFP7 brachydanio
12	822	36.9	422	2 Q81XW4	Q81XW4 homo sapien
13	816	36.7	388	1 P2X4 HUMAN	Q99571 homo sapien
14	813	36.5	388	2 Q8NA1	Q8NA1 homo sapien
15	803.5	36.1	421	1 P2X5 HUMAN	Q93086 homo sapien
16	795	35.7	388	2 Q92257	Q92257 mus musculu
17	795	35.7	388	2 Q9JUX6	Q9JUX6 mus musculu
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23	785	35.3	391	2 Q9DDP1	Q9DDP1 xenopus lae
24	777	34.9	391	2 Q9DDP1	Q9DDP1 xenopus lae
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26	755	33.9	389	2 Q6NVR1	Q6NVR1 brachydanio
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28	754	33.9	389	2 Q9ETZ0	Q9ETZ0 brachydanio
29	744	33.4	399	1 P2X1 HUMAN	P51575 mus musculu
30	740	33.2	399	1 P2X1 MOUSE	P51576 mus musculu
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ALIGNMENTS

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DT	15-DEC-1998 (Rel. 37, Last sequence update)				F47824 rattus norv
DT	05-JUL-2004 (Rel. 44, Last annotation update)				Aah61742 rattus no
DB	P2X purinoceptor 6 (ATP receptor) (P2X6) (Purineric receptor) (P2XM)				C9awc8 brachydanio
DB	(Purineric receptor P2X-like 1).				Q70397 cavia porce
GN	Name=P2X6L1; Synonyms=P2X6, P2X6;				Q8awc0 gallus gall
OS	Homo sapiens (Human).				Q7szl7 brachydanio
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RX	MEDLINE=97384966; PubMed=9242461;				Q8k3p1 mus musculu
RA	Urano T., Nishimori H., Han H., Furuhashi T., Kimura Y., Nakamura Y.,				Q78dw3 rattus norv
RA	Tokino T.;				
RT	"Cloning of P2XM, a novel human P2X receptor gene regulated by p53."				
RL	Cancer Res. 57:3281-3287(1997).				
RN	[2]				
RC	SEQUENCE FROM N.A.				
RA	TISSUE=Skeletal muscle;				
RT	Cheng X., Jin H., Huang C.-C.;				
RT	"Cloning and tissue distribution of a human cDNA encoding P2X6				
RL	purinoceptor.";				
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.				
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RX	MEDLINE=22107313; PubMed=12112843;				
RX	DOI=10.1002/1515-9861(200206)2:5<642::AID-PROT642>3.0.CO;2-I;				
RA	Maguire P.B., Wynne K.J., Harney D.F., O'Donoghue N.M., Stephens G.,				
RA	Fitzgerald D.J.;				
RT	"Identification of the phosphotyrosine proteome from thrombin				
RT	activated platelets.";				
RL	Proteomics 2:642-648(2002).				
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CC	(By similarity).				
CC	-1- SUBUNIT: Homo- or heteropolymers (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- TISSUE SPECIFICITY: Expressed predominantly in skeletal muscle.				
CC	-1- SIMILARITY: Belongs to the P2X receptor family.				
CC					
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC					
DR	EMBL; AB002059; BAA22047.1; -				
DR	EMBL; AB002058; BAA22046.1; -				

DR EMBL; AF065385; AAFL1303.1; -;
 DR Genew; HGNC:8538; P2RXL1.
 DR MIM; 608077; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0015267; F: channel/pore class transporter activity; TAS.
 DR GO; GO:0004888; F: transmembrane receptor activity; TAS.
 DR GO; GO:0006936; P: muscle contraction; TAS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR GO; GO:0006810; P: transport; TAS.
 DR InterPro; IPR001429; P2X_receptor.
 DR Pfam; PF00864; P2X_receptor; 1.
 DR PRINTS; PRO1307; P2XRECEPTOR.
 DR TIGRFAMs; TIGR00863; P2X; 1.
 DR PROSITE; PS01212; P2X RECEPTOR; 1.
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 KW Transmembrane.
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 DB 301 RTLKLYGIRFDILVTGQAGKFGLIPTAVTGTGAAMLGVVTFPCDLLLLLYVDREAHFYW 360
 QY 335 RTKYEAKAPKATANSVMRELALASQARLAELCLRRSSAPAPTATAAGSQTOTPGWPCPSS 394
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 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE P2RXL1 protein.

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 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.
 RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J.,
 RA Beare D.M., Dunham I.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: Homo- or heteropolymers (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the P2X receptor family.
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 DR InterPro; IPR003049; P2X6_purinocceptor.
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 DR Pfam; PF00864; P2X_receptor; 1.
 DR PRINTS; PRO1313; P2X6RECEPTOR.
 DR PRINTS; PRO1307; P2XRECEPTOR.
 DR TIGRFAMs; TIGR00863; P2X; 1.
 DR PROSITE; PS01212; P2X RECEPTOR; 1.
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 KW Transport.
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 DB 431 DTHLPTHSGSL 441

RESULT 3

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 AC CAG30421;
 DT 01-JUN-2004 (TrEMBLrel. 27, Created)
 DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
 DE P2RXL1 protein.
 GN P2RXL1.
 OS Homo sapiens (Human).

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervical ganglion;
 RX MEDLINE=96256686; PubMed=8786426;
 RA Collo G., Kawashima E., Pich E., Neidhart S., North R.A.,
 RA Surprenant A., Buell G.N.,
 RT "Cloning of P2X5 and P2X6 receptors and the distribution and
 RT properties of an extended family of ATP-gated ion channels.";
 RL J. Neurosci. 16:2495-2507(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=96264662; PubMed=8670303;
 RA Soto F., Garcia-Guzman M., Karschin C., Stuehmer W.,
 RT "Cloning and tissue distribution of a novel P2X receptor from rat
 RT brain.";
 RL Biochem. Biophys. Res. Commun. 223:456-460(1996).
 CC -!- FUNCTION: Receptor for ATP that acts as a ligand gated ion
 CC channel.
 CC -!- SUBUNIT: Homo- or heteropolymers (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the P2X receptor family.
 CC
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 CC
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 DR EMBL; X97376; CA66044.1; -;
 DR PIR; JC4843; JC4843.
 DR RGD; 3243; P2rx11.
 DR InterPro; IPR001429; P2X_receptor.
 DR Pfam; PF00864; P2X_receptor; 1.
 DR PRINTS; PR01307; P2XRECEPTOR.
 DR TIGRFS; TIGR00863; P2X; 1.
 DR PROSITE; PS01212; P2X_RECEPTOR; 1.
 DR GlycoProtex; Ion transport; Ionic channel; Receptor; Transmembrane.
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 FT DOMAIN 53 325
 FT TRANSMEM 326 346
 FT DOMAIN 347 379
 FT CARBOHYD 157 157
 FT CARBOHYD 187 187
 FT CARBOHYD 202 202
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 368 EAKAPKATNS 378
 Db QY 12 LDYKTEK-----WALLAKGYQERDLEPQFSIITKLKG 45
 Db 13 LFDYKTEKVIANKKVGILYRWQLSILAYLVGVVFWVVKGYQDITSLQSVITKLKG 72
 QY 46 VSVTQIKELGNRLMDVADFKVPQGENVFLVTFNLTVAQVQGRCPHPSPVPLANCWD 105
 Db 73 VAFNTSELGERLMDVADFKVPQGENVFLVTFNLTVAQVQGRCPHPSPVPLALCHQD 132
 QY 106 EDCPEGEGTHSHGVKTCGVVFNTHRTCEIWSHCPVSGVSPRPILLAAQNFTLFI 164
 Db 133 EDCPEGAQVAVNGVKTGRCLKDRDSIRGSCVLAWCVPVEKSKPKKPLLAENFTVFI 192

QY 165 KNTVTSKFNFSKNALETWPTFKHCRYPQSPYCFVFRIGDLVAKAGTGFEDLALL 224
 DB 193 KNSIRFPKFNFSKNTVRDTKGSPLKTCRHSKD-DHYCFIPLGLKIVSWSGSDFOIDALE 251
 QY 225 GSGVIRVHWDCLDTGSGCWPHYSF-----QIQEKS-----YNFRATHWEOFGVEAR 275
 DB 252 GGVIGIQIEWDCNLDKDASECHPRYSFTRLDNKFSEKSVSGYNFRYAKYRYDYNEDYR 311
 QY 276 TLLKLYGRFDILVTOGQKFLIPTAVTLTGGAWLGVWTFPFCDDLLLYVDREAHFVWR 335
 DB 312 TLIKAYGIRFDIWMVGKAGKFNIIITINISGLALMGAGAFCDLVLLYVYKRSFYRD 371
 QY 336 KYEBKAPK 345
 DB 372 KFEVGVSKV 381

RESULT 9

P2X5 RAT
 ID P2X5 RAT STANDARD; PRT; 455 AA.
 AC P51578; Q64613;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE P2X5 purinoceptor 5 (ATP receptor) (P2X5) (Purinergic receptor).
 GN Name=P2rx5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Coeliac ganglion;
 RX MEDLINE=96256686; PubMed=8786426;
 RA Collo G.Y., Kawashima B., Pich E., Neidhart S., North R.A.,
 RA Surprenant A., Buell G.N.,
 RT "Cloning of P2X5 and P2X6 receptors and the distribution and
 RT properties of an extended family of ATP-gated ion channels."
 RL J. Neurosci. 16:2495-2507(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Heart;
 RX MEDLINE=96275514; PubMed=8690069;
 RA Garcia-Guzman M., Soto F., Laube B., Stuehmer W.,
 RT "Molecular cloning and functional expression of a novel rat heart P2X
 RT purinoceptor."
 RL FEBS Lett. 388:123-127(1996).
 CC -!- FUNCTION: Receptor for ATP that acts as a ligand gated ion
 CC channel.
 CC -!- SUBUNIT: Homo- or heteropolymers (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in heart but are also
 CC present in brain, spinal cord and adrenal gland.
 CC -!- SIMILARITY: Belongs to the P2X receptor family.
 CC
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 CC
 CC EMBL; X92069; CAA63052.1; -
 CC EMBL; X71328; CAA65993.1; -
 CC PIR; S71344; S71344.
 CC RGD; 620256; P2rx5.
 CC InterPro; IPR001429; P2X_receptor.
 CC Pfam; PF00864; P2X_receptor; 1.
 CC PRINTS; PR01307; P2XRECEPTOR.
 CC TIGRFAMs; TIGR00863; P2X; 1.
 CC PROSITE; PS01212; P2X_RECEPTOR; 1.

KW Glycoprotein; Ion transport; Ionic channel; Receptor; Transmembrane.
 FT DOMAIN 1 30 Cytoplasmic (Potential).
 FT TRANSMEM 31 51 1 (Potential).
 FT DOMAIN 52 341 Extracellular, cysteine-rich (Potential).
 FT TRANSMEM 342 362 2 (Potential).
 FT DOMAIN 363 455 Cytoplasmic (Potential).
 FT CARBOHYD 77 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 157 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 202 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 191 S -> F (in Ref. 2).
 FT CONFLICT 396 R -> Q (in Ref. 2).
 FT SEQUENCE 455 AA; 51479 MW; D4405BB440490F70 CRC64;
 Query Match 40.1%; Score 892; DB 1; Length 455;
 Best Local Similarity 46.6%; Pred. No. 66-73;
 Matches 174; Conservative 55; Mismatches 108; Indels 36; Gaps 5;
 QY 12 LLDYKTEK-----WALLAKGYQRDLQPPQSIITKLKG 45
 DB 13 LPDYKTAKFVVAKSKVGLLYRVLQLILLYLLIWLFLIKSYQDIDTSLQSAVTVKVG 72
 QY 46 VSVTOIKELGNRLWADVADVPKPPQGENVFFLVTNFLVTPAQVQGRCPHPSPVLANCWD 105
 DB 73 VAYTNTMLGERLWADVADVPISQGENVFFVTVNLTVPNQRQGI CAEREGIPDGECSB 132
 QY 106 EDCPEGEGETHSHGVKTCGV-VFNGTHRTCTIWMSCVPVSGVSPRLPAAQNFITLFI 164
 DB 133 DCHAGESVVAAGHLTKGRCLRVGNSTRCTGCFIFANCPVETKSMETDPLLDKDAESFTISI 192
 QY 165 KNTVTSKFNFSKNALETWPTFKHCRYPQSPYCFVFRIGDLVAKAGTGFEDLALL 224
 DB 193 KXFIKPFKFNFSKANVLETDNKHFLKTCFHS-STNLYCPFRLGSIVRWAGADFQDIALK 251
 QY 225 GGSVGRVHWDCLDTGDSGCWPHYSF-QIQEKS-----SYNFRATHWEOFGVEAR 276
 DB 252 GGVIGIQIEWDCDLDKDAKSCNPHYFNRLDNKHTHSISSGNFRFARYRDPNGVFERD 311
 QY 277 LKLYGIRFDILVTOGQKFLIPTAVTLTGGAWLGVWTFPFCDDLLLYVDREAHFVWR 336
 DB 312 LMKAYGIRFDIVNGKAGKFSIIPVINGISGLALMGAGAFCDLVLLYVYKRSFYRDK 371
 QY 337 KYEBKAPKATAN 349
 DB 372 KFEKVRGQKEDAN 384

RESULT 10

Q91VE2
 ID Q91VE2 PRELIMINARY; PRT; 455 AA.
 AC Q91VE2;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE ATP-gated ionotropic P2X5 receptor subunit.
 GN Name=P2rx5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ, and BALB/c; TISSUE=Heart;
 RX MEDLINE=21297188; PubMed=11404011;
 RA Cox J.A., Barmina O., Voigt M.M.,
 RT "Gene structure, chromosomal localization, cDNA cloning and expression
 RT of the mouse ATP-gated ionotropic receptor P2X5 subunit."
 RL Gene 270:145-152(2001).
 CC -!- SUBUNIT: Homo- or heteropolymers (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the P2X receptor family.
 CC EMBL; AF333333; AAK49937.1; -
 CC EMBL; AF333332; AAK49937.1; JOINED.
 CC EMBL; AF333331; AAK49936.1; -.

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Homo- or heteropolymers (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the P2X receptor family.
DR EMBL; BC039015; AAH39015.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR003048; P2X5_purinocptor.
DR InterPro; IPR001429; P2X_receptor.
DR Pfam; PF00864; P2X_receptor; 1.
DR PRINTS; PR01312; P2XSRECEPTOR.
DR PRINTS; PR01307; P2XRECEPTOR.
DR TIGRFAMs; TIGR00863; P2X; 1.
DR PROSITE; PS01212; P2X RECEPTOR; 1.
KW Glycoprotein; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 422 AA; 47204 MW; B122027A3B2A240 CRC64;

Query Match 36.9%; Score 822; DB 2; Length 422;
Best Local Similarity 40.3%; Pred. No. 1.5e-66;
Matches 173; Conservative 60; Mismatches 120; Indels 76; Gaps 9;

QY 12 LLDYKTEK-----WALLAKYQERDELPQFSITKLKG 45
DB 13 LFDYKTEKVIANKKVGILLYLLOASILAYLVWVFLIKGYQDVDTLSQSAVITKVG 72

QY 46 VSVTQIKELGNLWDVADVPKPPQGENVFFLTNPLVPAQVQGRCPHPSPVLANCWD 105
DB 73 VAFVTSDLGQRINDVADVIVIAQGENVFFVTVNLIVPNQGVNCAENEGIPDGACSKD 132

QY 106 EDCPEGEQTHGHVTKGCVFNGVTHR-TCIHWNCVPSGVSPRPELLAQONFLFI 164
DB 133 SDCHAGEAVTAGNKGKTRCLRENLAGTCTIFAWCPLTSSRPEEPFLKEADFTFI 192

QY 165 KNTVTFSEKFNFSKNALETWDPTEFKHCRYPQFSPVFRIGDLVAKAGTDEDIAL 224
DB 193 KKHIRPPKFNFSKNVMDVKRSFLKSHFGPK-NHYCPIFLGSVIVWAGSDQDIALE 251

QY 225 GGSVGIRVHWCDDLTGDSGCWPHYSF-QLQEK-----SYNFRATHWEPQVEART 276
DB 252 GGVIGINIENWCDDKAASECHPHYSFSGRLDNKLSKSVSSGYNFRFARYRDAAGVEPT 311

QY 277 LKLKVGIRFDILVTGQAGKFGILPVTAVLTGTGAAMLGVVTFPCDLLLYVDREAHFYWT 336
DB 312 LMKAVGIRFDVWNGK-----AFFCDLVLYLKKREFYRDK 349

QY 337 KYEEKAPKATANSVWRELALASQARLACPLRRSSAPA-----PTATAAGSQ 383
DB 350 KYEEVRGLEDSQEADE--ASGLGLSEQL--TSGPGLLGMPEQQLQEPPEAKRGSSS 404

QY 384 TQTPGWPCCP 392
DB 405 QKNGSVCP 413

RESULT 13
P2X4_HUMAN STANDARD; PRT; 388 AA.
ID P2X4_HUMAN Q9571; O00450; O14722; Q9UBG9;
AC Q9571; O00450; O14722; Q9UBG9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE P2X purinoreceptor 4 (ATP receptor) (P2X4) (Purinergic receptor).
GN Names=P2RX4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97168759; PubMed=9016352;
RA Garcia-Guzman M., Soto F., Gomez-Hernandez J.M., Lund P.E.,
RA Stuhmer W.;
RT "Characterization of recombinant human P2X4 receptor reveals
RT pharmacological differences to the rat homologue.";
RL Mol. Pharmacol. 51:109-118(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamagata K., Oda N., Furuta H., Vaxillaire M., Souham L., Boriraj V.,
RA Chen X., Oda Y., Takeda J., Yamada S., Nishigori H., Lebeau M.M.,
RA Lathrop M., Cox R.D., Bell G.I.;
RT "Transcription map of the 5CM region surrounding the hepatocyte
RT nuclear factor-1a/MODY3 gene on chromosome 12.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Korenaga R., Yamamoto K., Kamiya A., Ando J.;
RT "Shear stress downregulates the expression of P2X4 receptor by human
RT endothelial cells.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 35-388 FROM N.A.
RA Takahashi K., Korenaga R., Kamiya A., Ando J.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 73-326 FROM N.A.
RC TISSUE=Kidney;
RA Chang A.S., Chang S.M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for ATP that acts as a ligand gated ion
CC channel. This receptor is insensitive to the antagonists PPADS and
CC suramin.
CC -!- SUBUNIT: Homo- or heteropolymers (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the P2X receptor family.
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CC EMBL; Y07684; CAA68948.1; -;
DR EMBL; U87270; AAD00556.1; JOINED.
DR EMBL; U85971; AAD00556.1; JOINED.
DR EMBL; U85972; AAD00556.1; JOINED.
DR EMBL; U85973; AAD00556.1; JOINED.
DR EMBL; U85974; AAD00556.1; JOINED.
DR EMBL; U85975; AAD00556.1; JOINED.

DR EMEL; U83993; AAD00553.1; --
 DR EMEL; AF191093; AAR06661.1; --
 DR EMEL; AF000234; AAB58405.1; --
 DR EMEL; AF012903; AAB66834.1; --
 DR Genew; HGNC:8535; P2RX4.
 DR MIM; 600846; --
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004931; F: ATP-gated cation channel activity; TAS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR GO; GO:0006810; P: transport; TAS.
 DR InterPro; IPR001429; P2X receptor.
 DR Pfam; PF00864; P2X receptor; 1.
 DR PRINTS; PRO1307; P2XRECEPTOR.
 DR TIGRFAMS; TIGR00863; P2X; 1.
 DR PROSITE; PS01212; P2X_RECEPTOR; 1.
 DR Glycoprotein; ion transport; Ionic channel; Polymorphism; Receptor; Transmembrane.
 KW DOMAIN 1 33 Cytoplasmic (Potential).
 FT TRANSMEM 34 54 1 (Potential).
 FT DOMAIN 55 338 Extracellular, cysteine-rich (Potential).
 FT TRANSMEM 339 359 2 (Potential).
 FT DOMAIN 360 388 Cytoplasmic (Potential).
 FT CARBOHYD 75 75 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 153 153 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 208 208 N-linked (GlcNAc...) (Potential).
 FT VARIANT 242 242 S->G (in dbSNP:25644).
 FT /FTID=VAR_014942.
 FT CONFLICT 6 6 S->A (in Ref. 2).
 FT CONFLICT 121 121 D->S (in Ref. 5).
 FT CONFLICT 148 148 R->W (in Ref. 5).
 FT CONFLICT 179 179 L->P (in Ref. 5).
 FT CONFLICT 238 238 N->I (in Ref. 5).
 FT CONFLICT 315 315 Y->C (in Ref. 4).
 SQ SEQUENCE 388 AA; 43385 MW; 3681E192E9CF201E CRC64;
 Query Match 36.7%; Score 816; DB 1; Length 388;
 Best Local Similarity 47.0%; Pred. No. 4.7e-66;
 Matches 155; Conservative 56; Mismatches 107; Indels 12; Gaps 4;
 QY 20 WALLAKKGQERDLFPQFSIIITKLKGVSVTQIKELGNRLWDVADVPKPGQGNVFLVTN 79
 Db 45 WYFVMEKGYQETD-SVVSSTTKVKGAVTNTSKLGFRIWDVADYVIPAQENSFLVMTN 104
 QY 80 FLVTPAQVQGRCPHPSPVLANCWVDEDCPEGGTSHGVKTCQVFNQTHRTCEIWS 139
 Db 105 VILTMNQTQGLCPETDATTVCXSDASCTAGSAGTHNGVSTGRVAFNGSVKTCVAA 163
 QY 140 WCPVESGV-VPSRPLLAQAQNTFLFKNTVTSKFNFSKNALETWDPDYFKHCRYPQF 198
 Db 164 WCPVEDDTHVPQAPFLKAAENFTLLVKNINWPKFNFSKRNILPNITTYLKSICYDAKT 223
 QY 199 SPYCPVFRIGDLVAKGTFEDLALLGSGVGRVHWDCLDTGDSGCPHYSFQLOE--- 255
 Db 224 DFCFCIFRLKIVENAGHSFQDAVEGGIMGVQVNDCLDRAELCLPRYSFRRLDTRD 283
 QY 256 -----KSNFRATATHWQEQVEARTLLKLYGIRFDILVTGQAGKGLIPTAVTLGFGA 309
 Db 284 VEHNVSPGYNFRFAKYRDLAGNEQRTLLIKAYGIRFDIIVFGKAGKGLIPTMINISGL 343
 QY 310 AWLGVTTFCDLLLVYDREAHFYRTKYE 339
 Db 344 ALLGMATVLCIDIIVLYCMKGRLYYREKYK 373
 RESULT 14
 Q8N4N1 PRELIMINARY; PRT; 388 AA.
 ID Q8N4N1
 AC Q8N4N1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT EMEL; U83993 (TrEMBLrel. 25, Last annotation update)
 DE Purinergic receptor P2X4, isoform a.
 GN Name=P2RX4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: Homo- or heteropolymers (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the P2X receptor family.
 DR EMEL; BC033826; AAB33826.1; --
 DR PIR; JC6543; JC6543.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005524; F: ATP binding; IEA.
 DR GO; GO:0005216; F: ion channel activity; IEA.
 DR GO; GO:0004872; P: receptor activity; IEA.
 DR GO; GO:0006811; P: ion transport; IEA.
 DR InterPro; IPR003047; P2X4_purinocceptor.
 DR InterPro; IPR001429; P2X_receptor; 1.
 DR Pfam; PF00864; P2X_receptor; 1.
 DR PRINTS; PRO1311; P2X4RECEPTOR.
 DR PRINTS; PRO1307; P2XRECEPTOR.
 DR TIGRFAMS; TIGR00863; P2X; 1.
 DR PROSITE; PS01212; P2X_RECEPTOR; 1.
 DR Glycoprotein; ion transport; Ionic channel; Receptor; Transmembrane; Transport.
 KW SEQUENCE 388 AA; 43339 MW; AF7ABC688FCE02A5 CRC64;
 Query Match 36.5%; Score 813; DB 2; Length 388;
 Best Local Similarity 47.0%; Pred. No. 8.8e-66;
 Matches 155; Conservative 55; Mismatches 108; Indels 12; Gaps 4;
 QY 20 WALLAKKGQERDLFPQFSIIITKLKGVSVTQIKELGNRLWDVADVPKPGQGNVFLVTN 79
 Db 46 WYFVMEKGYQETD-SVVSSTTKVKGAVTNTSKLGFRIWDVADYVIPAQENSFLVMTN 104
 QY 80 FLVTPAQVQGRCPHPSPVLANCWVDEDCPEGGTSHGVKTCQVFNQTHRTCEIWS 139
 Db 105 VILTMNQTQGLCPETDATTVCXSDASCTAGSAGTHNGVSTGRVAFNGSVKTCVAA 163
 QY 140 WCPVESGV-VPSRPLLAQAQNTFLFKNTVTSKFNFSKNALETWDPDYFKHCRYPQF 198
 Db 164 WCPVEDDTHVPQAPFLKAAENFTLLVKNINWPKFNFSKRNILPNITTYLKSICYDAKT 223

Db 349 KYEEVRGLEDSSQEADE---ASGLGLSEQL--TSGPGLLGMPQQELQEPPEAKRGSS 403

Qy 384 TQTEGWPCP 392

Db 404 QKNGSVCP 412

Search completed: November 21, 2004, 15:03:29
Job time : 193 secs

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OM protein - protein search, using sw model

Run on: November 21, 2004, 14:54:02 ; Search time 40 Seconds
(Without alignments)
974.195 Million cell updates/sec

Title: US-09-820-095B-2
Perfect score: 2226
Sequence: 1 MGSPGATTGWLDDYKTEK.....TPGWPCSSDTHLPTSGSL 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
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4: pir4:.*

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1554	69.8	379	JC4843	ATP-gated ionchann
2	900	40.4	455	S71344	purinergic recepto
3	815	36.6	388	JC6543	P2X4 receptor - hu
4	793	35.6	388	JC6137	ATP-gated ion chan
5	744	33.4	399	S71327	ATP-gated ion chan
6	739	33.2	339	S50860	apoptosis protein
7	720	32.3	472	S50859	P2X receptor - rat
8	679.5	30.5	397	S60334	purinoceptor P2X -
9	679.5	30.5	397	I58099	gene P2X3 protein
10	96.5	4.3	562	B91194	probable enzyme (i
11	96.5	4.3	562	C86041	probable enzyme yi
12	95	4.3	372	T47344	hypothetical prote
13	95	4.3	1036	F71565	probable isoleucin
14	94.5	4.2	562	A65166	hypothetical 63.2K
15	94.5	4.2	628	I38000	lutheran blood gro
16	92.5	4.2	588	I37202	B-CAM protein - hu
17	91.5	4.1	392	I54491	cell surface antig
18	90	4.0	844	C91212	probable outer mem
19	90	4.0	844	C86058	probable fibrial
20	89.5	4.0	1025	A43526	complement C3d/Bps
21	88	4.0	3947	T52486	ferrichrome sidero
22	87	3.9	6658	T13931	projectin - fruit
23	86.5	3.9	618	T00476	probable vacuolar
24	86.5	3.9	737	S65758	nitrate reductase
25	86	3.9	375	A32827	fetuin precursor -
26	85.5	3.8	1743	T28859	hypothetical prote
27	85	3.8	806	A35963	protein-tyrosine k
28	84.5	3.8	282	JC5439	D-aspartate oxidas
29	84.5	3.8	341	JC5438	D-aspartate oxidas

30	84.5	3.8	559	1	A35029	t-plasminogen acti
31	84.5	3.8	995	2	C83203	probable serine pr
32	84	3.8	561	2	A25090	chitinase (EC 3.2.
33	83.5	3.8	635	2	A45266	MPL-P protein prec
34	83.5	3.8	1036	2	F81719	isoleucyl-tRNA syn
35	83.5	3.8	1367	2	T21913	hypothetical prote
36	83	3.7	347	2	T08371	probable UDP-glucu
37	83	3.7	364	2	AE3196	conserved hypothet
38	83	3.7	713	1	S30019	acetate-CoA ligase
39	83	3.7	881	2	AD2580	two component sens
40	83	3.7	881	2	C97362	protein sensor pro
41	83	3.7	1049	2	T30525	alpha-mannosidase
42	82.5	3.7	164	2	H95889	phosphoesterase-re
43	82.5	3.7	508	2	S41879	readthrough protei
44	82.5	3.7	746	2	AC1883	nitrate reductase
45	82.5	3.7	1344	2	S47412	gene P2 protein -

ALIGNMENTS

RESULT 1

JC4843

ATP-gated ionchannel receptor, P2X6 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004

C:Accession: JC4843

R:Solto, F.; Garcia-Guzman, M.; Karschin, C.; Stuehmer, W.

Biochem. Biophys. Res. Commun. 223, 456-460, 1996

A:Title: Cloning and tissue distribution of a novel P2X receptor from rat brain.

A:Reference number: JC4843; MUID:96264662; PMID:8670303

A:Contents: brain

A:Accession: JC4843

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-379 <SOT>

A:Cross-references: UNIPROT:P51579; GB:X97376; NID:g1419751; PIDN:CAA66044.1; PID:g14197

C:Comment: This receptor is a ATP-gated ion channel.

C:Superfamily: ATP-gated ion channel P2X4 receptor

C:Keywords: brain; glycoprotein; receptor; transmembrane protein

F30-52/Domain: transmembrane #status predicted <TM1>

F330-355/Domain: transmembrane #status predicted <TM2>

F:157,187,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	69.8%;	Score 1554;	DB 2;	Length 379;
Best Local Similarity	75.7%;	Pred. No. 7.2e-130;		
Matches 281;	Conservative 26;	Mismatches 38;	Indels 26;	Gaps 1;
QY	6	ATTGWLGLLDYKTEK-----	WALLAKGYQERDLEPQFSI	39
DB	8	ALVSWGFLDYKTEKYVMTRNCWVGISQRLQLGVVVVIGWALLAKGYQEWMDPQISV	67	
QY	40	ITKLKGVSVTQIKELGNRLMDVADVPQGENVFFLVTFNPLVTPPAQVQGRCPHPSPVL	99	
DB	68	ITKLKGVSVTQVKELEKRLMDVADVPQSGENVFFLVTFNPLVTPPAQVQGRCPHPSPVL	127	
QY	100	ANCWVDEDCPGEGETHSHGVKTCQCQVFNFGTHRTCTIWSMCPVSVGVPSPRLAAQON	159	
DB	128	ANCWADEDCPGEGETHSHGKTCQCVAFNGTHRTCTIWSMCPVSVSAVPRKPIAQAQN	187	
QY	160	FTLPIKNTVTPFSKFNFSKNALETWDTPTFKHCRYEPQFSPYCPVFRIGDLVAKAGTTEE	219	
DB	188	FTLPIKNTVTPFNKFNFSRTWALDTWNTYFKYCLYDLSLSPYCPVFRIGDLVAMTGGDFE	247	
QY	220	DLALLGSGVGRVHWDCCDLDTGDSGCWPHYSFQLOEKSYNFRCTATHWEGPQVEARTLLK	279	
DB	248	DLALLGSAVGINIHWCNCLDTKSDCSQPSYFQLOERGVNFRNTANYWAAASGVESRLLK	307	
QY	280	LYGIRFDILVTQAGKFGFLIPTAVTLTGTGAALGWVTFPCDLLLLYYDRAHFYWRITKYE	339	
DB	308	LYGIRFDILVTQAGKFGFLIPTAVTLTGTGAALGWVTFPCDLLLLYYDRAHFYWRITKYE	367	
QY	340	EAKAPKATANS 350		

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Db 368 EAPAPKATNS 378
|||||
RESULT 2
S71344
purinergic receptor P2X5 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S71344
R:Garcia-Guzman, M.; Soto, F.; Laube, B.; Stuehmer, W.
FEBS Lett. 388, 123-127, 1996
A>Title: Molecular cloning and functional expression of a novel rat heart P2X purinoceptor
A:Reference number: S71344; MUID:96275514; PMID:8690069
A:Accession: S71344
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-455 <GAR>
A:Cross-references: UNIPROT:P51578; EMBL:X97328; NID:g1419749; PIDN:CAA65993.1; PID:g1419749
A:Experimental source: heart
C:Genetics:
A:Gene: P2X5
C:Superfamily: ATP-gated ion channel P2X4 receptor
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:29-51/Domain: transmembrane #status predicted <TM1>
F:337-362/Domain: transmembrane #status predicted <TM2>
F:18,149/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:26,158/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:77,157,202/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 40.4%; Score 900; DB 2; Length 455;
Best Local Similarity 46.9%; Pred. No. 8.9e-72; Indels 36; Gaps 5;
Matches 175; Conservative 55; Mismatches 107;
QY 12 LLDYKTEK-----WALLAKGYQERDLEPQPSIITKLG 45
Db 13 LPDYKTAQFVAKSKVGLLYRVQLIILLYLLIWLKLYQIDITSLQSAVTVKVG 72
QY 46 VSVTQIKELGNRLWDVADFKVPPQGENVFVLTNLFVTPAQVQGRCPHSPVPLANCWD 105
Db 73 VAYNTTMLGERLWDVADFKVPPQGENVFVLTNLFVTPAQVQGRCPHSPVPLANCWD 132
QY 106 EDCPEGGTHSHGVKTGCY-VFNGTHETCEIWSMCPVSGVPSRPLLAQAQNTLFI 164
Db 133 DDCHAGESVAGGLTKGCLRVNGSTRGTCTEIFAWCPVETKSMPTDPLDKAESFTLFI 192
QY 165 KNTVTFSKFNFSKNALETWDPYFKHCRYEPQSPYCPVFRIGDLVAKAGTFFEDLALL 224
Db 193 KNFIRPKFNFSKANVLETDNKHFLKXTCHFS-STNLYCPIFLGSIVRWAGADFQDIALK 251
QY 225 GGSVGIRVHWDCDLTDGSCWPHYSF-QLOEK-----SYNERTATHWQPGVEART 276
Db 252 GGVIGVIEWDCDLDAASKNCPHYFNRLDNKHTSISSGNFRFARYRDPNGVEPR 311
QY 277 LLKLYGIRFDILVTGQAGKFGLLIPTAVLTGTGAALGVVTFCDLLLYVDREAHFYRT 336
Db 312 LMKAYGIRFDIVNGKAGKFSIPTVINIGSGLALMGAGAFFCDLVLIIRKSEFYRDK 371
QY 337 KYEAKAPKATAN 349
Db 372 KFEKVRGQKEDAN 384
RESULT 3
JC6543
P2X4 receptor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: JC6543
R:Dhulipala, P.D.K.; Wang, Y.X.; Kotlikoff, M.I.
Gene 207, 259-266, 1998
A>Title: The human P2X4 receptor gene is alternatively spliced.
A:Reference number: JC6543; MUID:98172760; PMID:9511769
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A:Accession: JC6543
A:Molecule type: mRNA
A:Residues: 1-388 <DHU>
A:Cross-references: UNIPROT:Q8N4N1
A:Experimental source: stomach
C:Comment: This receptor is an ATP requiring ion channel. It mediates membrane depolariza
C:Genetics:
A:Gene: P2X4
A:Introns: 95/3
C:Superfamily: ATP-gated ion channel P2X4 receptor
C:Keywords: glycoprotein; ion channel; receptor
F:30-50/Domain: transmembrane #status predicted <TM1>
F:338-361/Domain: transmembrane #status predicted <TM2>
F:75,110,153,184,199,287/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 36.6%; Score 815; DB 2; Length 388;
Best Local Similarity 47.0%; Pred. No. 2.5e-64;
Matches 155; Conservative 56; Mismatches 107; Indels 12; Gaps 4;
QY 20 WALLAKGYQERDLEPQPSIITKLGYSVTQIKELGNRLWDVADFKVPPQGENVFVLTN 79
Db 46 WVFVWEKGYQETD-SVYSSVTTKVKGAVTNTSKLGRFDVADYVIPAQKENSFLVMTN 104
QY 80 FLVTPAQVQGRCPHSPVPLANCWDPCPEGGGTHSHGVKTGCWFWNGTHRTCEIWS 139
Db 105 VILTMNQTQGLCEIPDAITV-CKSDASCTAGSAGTHSGVSTGRCVAFNGSVKTCVAA 163
QY 140 WCPVESGV-VPSRPLLAQAQNTLFIKNTVTFSKFNFSKNALETWDPYFKHCRYEQF 198
Db 164 WCPVEDDTHVQPAFLKAAENFTLLVKNINWIYKFNFSKRNILFNTTTLKSCIYDAKT 223
QY 199 SPYCPVFRIGDLVAKAGTFFEDLALGSGVIGIRVHWDCDLTDGSCWPHYSFQLOE--- 255
Db 224 DPCPIPRFKIIVENAGHSFQDMVAVKGGINGIQVWDCNLDRAASLCLPRYSFRLEDTR 283
QY 256 -----KSNFRFATHWQPGVGEARTLLKLYGIRFDILVTGQAGKFGLLIPTAVLTGCA 309
Db 284 VEHNVSPGVNFRFAKYVRDLAGNEQRTLIKAYGIRFDIIVFGKAGKFDIIPMTINIGSGL 343
QY 310 AWLGVTFFCDLLLYVDREAHFYRTKYE 339
Db 344 ALLGMSTVLCIDIIVLYCMKRLIYREKKYK 373
RESULT 4
JC6137
ATP-gated ion channel P2X4 - rat
N:Alternate names: ATP-activated ionotropic receptor P2X4; P2X4 purinoreceptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JC6137; JC4684; S6206; S72563; S62359
R:Soto, F.; Garcia-Guzman, M.; Gomez-Hernandez, J.M.; Hollmann, M.; Karschin, C.; Stuehme
Proc. Natl. Acad. Sci. U.S.A. 93, 3684-3688, 1996
A>Title: P2X4: An ATP-activated ionotropic receptor cloned from rat brain.
A:Reference number: JC6137; MUID:96195033; PMID:8622937
A:Contents: brain
A:Accession: JC6137
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-388 <SOT>
A:Cross-references: UNIPROT:P51577; EMBL:X93565; NID:g1325958; PIDN:CAA63778.1; PID:g1325958
R:Wang, C.Z.; Namba, N.; Gonoi, T.; Inagaki, N.; Seino, S.
Biochem. Biophys. Res. Commun. 220, 196-202, 1996
A>Title: Cloning and pharmacological characterization of a fourth P2X receptor subtype wj
A:Reference number: JC4684; MUID:96176979; PMID:8602843
A:Accession: JC4684
A:Molecule type: mRNA
A:Residues: 1-388 <GB>
A:Cross-references: GB:U47031; NID:g1184996; PIDN:AAA99777.1; PID:g1184997
A:Experimental source: pancreatic islet
R:Bo, X.; Zhang, Y.; Naessar, M.; Burnstock, G.; Schoeffer, R.
FEBS Lett. 375, 129-133, 1995
A>Title: A P2X purinoceptor cDNA conferring a novel pharmacological profile.
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A;Cross-references: UNIPROT:P51575; EMBL:U45448; NID:gl314356; PIDN:AA05698.1; PID:gl313713

C;Genetics:

A;Map position: 17

C;Superfamily: ATP-gated ion channel P2X4 receptor

Query Match 33.4%; Score 744; DB 2; Length 399;

Best Local Similarity 44.0%; Pred. No. 5.1e-58;

Matches 159; Conservative 56; Mismatches 128; Indels 18; Gaps 9;

QY 20 WALLAKKGQYQERDLEPQFSIITKIKGVSVTQIKELGNRLWDVADFKPPQGGENVFFLVTN 79

DB 47 WVFLEYKGYQTSS-GLISSVSVKLGLAVTQLPGLGPQWDVADYVFPAGGDNSEFVMTN 105

QY 80 FLVTPAQVQRCDEHPSVPLANCWDEDCEPBGEGTHSGVKTGCQVWNGTHRTCEIWS 139

DB 106 FIYTPKQTGYCAEHPEGGI--CKEDSGTTPGAKRKAQGIIRTKCVATNDVTKTCEIFG 163

QY 140 WCQVE--SGVPSRPLLAQONFTLFIKNTVTSKFNFSKNALETWDPVTFKHCRYPEQF 198

DB 164 WCPVEVDDIIPRALRLREAENFTLFKNSISPRFKVNRNLVEEYNAAMTKCLPHKTL 223

QY 199 SPVCPVFRIGDLVAKAGGTFFEDIALGGSGVIRVHWDCLDTGDSGCWPHYSFQ--LQEK 256

DB 224 HPLCPVFQLGVYVQESQNFSTLAEXGGVVGITIDWHCDLDWHRVRCRPIYEFHGLYEK 283

QY 257 S-----NERTATHWQPGVGEARTLLKLGIRFDIILVTGQAGKFGLIPTAVTLGTGAWL 312

DB 284 NLSPGFNFRARFVEN-GTNVRLHFKVGIARFDIILVDGAKGFDIIPWTIIIGSIGIF 342

QY 313 GVTTFPCDLLLYVDREAHFY--WRTKYBEAKPKATANSVRELALASQA-RLAECLR 369

DB 343 GVATVLCDLLLHLIPKRHYVYQKPKYAEDMGPAE---RDLAATSSTLGLQENMRT 398

QY 370 S 370

DB 399 S 399

RESULT 6

S50860

apoptosis protein RP-2 - rat

N;Alternate names: gene P2X protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S50860; B41257

R;Valera, S.; Hussy, N.; Evans, R.J.; Adami, N.; North, R.A.; Surprenant, A.; Buell, G.

Nature 371, 516-519, 1994

A;Title: A new class of ligand-gated ion channel defined by P(2X) receptor for extracellular ATP

A;Reference number: S50860; MUID:95021691; PMID:7523951

A;Accession: S50860

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-399 <VAL>

A;Cross-references: UNIPROT:P47824; EMBL:X80477; NID:g558239; PIDN:CAA56647.1; PID:g558239

R;Owens, G.P.; Hann, W.E.; Cohen, J.J.

Mol. Cell. Biol. 11, 4177-4188, 1991

A;Title: Identification of mRNAs associated with programmed cell death in immature thymocytes

A;Reference number: A41257; MUID:91304410; PMID:2072913

A;Accession: B41257

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: FQLAKGYPCEPH', 202-399 <ONE>

A;Cross-references: GB:M80602; NID:g206713; PIDN:AAA42085.1; PID:g206714

C;Superfamily: ATP-gated ion channel P2X4 receptor

Query Match 33.2%; Score 739; DB 2; Length 399;

Best Local Similarity 43.8%; Pred. No. 1.4e-57;

Matches 153; Conservative 60; Mismatches 114; Indels 22; Gaps 8;

QY 20 WALLAKKGQYQERDLEPQFSIITKIKGVSVTQIKELGNRLWDVADFKPPQGGENVFFLV 78

DB 47 WVFLEYKGYQTSSDLTSSVS--KLKGLAVTQLGLGPQWDVADYVFPAGHDSSEFVMT 104

QY 79 NFLVTPAQVQGRCPHEPSVPLANCWVDBDCEGEGTHSHGKVTGCQCVFNGTHRTCEIW 138
Db 105 NFIVTPQQTQGHCAENPEGGI--CQDDSGCTPGKAERKAQGIKRGNCVFPNGVTKTCEIF 162
QY 139 SWCPVE-SGVVPSRPLLAQAQNFILFIKNTVTFKFNFSKNALETWDPYFKHCERYEPQ 197
Db 163 GWCPVEVDKIPSPALLREANFTLFIKNSIFRFKVNRRNLVEEVNGYMKKCLYHKI 222
QY 198 FSPYCPVFRIGDLVAKAGCTFEDLALLGSGVIRVHWDCCDLDTGDSGCWPHYSFQ--LQE 255
Db 223 QHPLCPVNLGVVRESQDPRSLAERKGVVGIIDMKCDLDMVHRCKPIYQPHGLYGE 282
QY 256 KS-----YNFRATHWHPGVEARTLLKLYGIRFDILVTGQAGKFGILPTAVLTGTAAN 311
Db 283 KNLSPGFNFRARH-FVQNGTNRRLHFKVFIHFDILVDGKAGKFDIPTMTTIGSGIGI 341
QY 312 LGVWTFPCDLLLLYVDREAHFYWRTKYEEAK-----APKATANSV 351
Db 342 FGVAIVLCDLLLLHILPRHYKQKKFYAEDMGPGGEHDPVATISSTL 390
RESULT 7
P2X4 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S50859
R:Brake, A.J.; Wagenbach, M.J.; Julius, D.
Nature 371, 519-523, 1994
A:Title: New structural motif for ligand-gated ion channels defined by an ionotropic AHP
A:Reference number: S50859; MUID:95021682; PMID:7523952
A:Accession: S50859
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <BRA>
A:Cross-references: UNIPROT:P49653; EMBL:U14414; NID:g558830; PIDN:AAA50756.1; PID:g5588
C:Superfamily: ATP-gated ion channel P2X4 receptor
Query Match 32.3%; Score 720; DB 2; Length 472;
Best Local Similarity 37.4%; Pred. No. 8.5e-56;
Matches 144; Conservative 71; Mismatches 144; Indels 26; Gaps 5;

QY 20 WALLAKGYQGRDLEPQPSIIITKLKGVSVTQIKELGNRLMDVADFKPKPGQGVNFFLVTN 79
Db 47 YVFIQKSYQDSQSGPSSIIITKVGITMSE----DKWMDVEYVYKPPGGSVSIIR 101
QY 80 FLVTPAQVQGRCPHEPSVPLANCWVDBDCEGEGTHSHGKVTGCQCV-FVNGTHRTCEIW 138
Db 102 IEVTPSQTLGTCPESMRVHSSTCHSDDDCIAGQDLMQNGIRTGCHVYVYHGSKTCEVS 161
QY 139 SWCPVESGVVPSRPLLAQAQNFILFIKNTVTFKFNFSKNALETWDPYFKHCERYEPQ 198
Db 162 ANCPVEDGTSNHLGLKWPAPNFTLFIKNSIHYPFKFSKGN-IAQSKSDYLKXCTPDQDS 220
QY 199 SPYCPVFRIGDLVAKAGCTFEDLALLGSGVIRVHWDCCDLDTGDSGCWPHYSFQLOE--- 255
Db 221 DPYCPVFRIGDLVAKAGCTFEDLALLGSGVIRVHWDCCDLDTGDSGCWPHYSFQLOE--- 255
QY 256 ----KSNFRATHWHPGVEARTLLKLYGIRFDILVTGQAGKFGILPTAVLTGTAAN 311
Db 281 DPASGYNFRFAKYKINGTTTTTLKAYGIRDIVHVGAGKFSILPIINLATLTS 340
QY 312 LGVWTFPCDLLLLYVDREAHFYWRTKYEEAKPKATANSVWRELASQARLAECRLRSS 371
Db 341 IGVGSFLCDWILLTFMKNKLYSHKKFDKVRTPKHPSRPVTLAV-----L 388
QY 372 APATATAGSQTQTPGHPCSSDT 396
Db 389 QOIPIPPPHSHYSQDQPPSPSGEGPT 413

RESULT 8
S60334

purinoceptor P2X - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Sep-1996 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C:Accession: S60334
R:Chen, C.C.; Akopian, A.N.; Sivilotti, L.; Colquhoun, D.; Burnstock, G.; Wood, J.N.
Nature 377, 428-435, 1995
A:Title: A P2X purinoceptor expressed by a subset of sensory neurons.
A:Reference number: S60334; MUID:96008544; PMID:7566119
A:Accession: S60334
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A:Molecule type: mRNA
A:Residues: 1-397 <CHE>
C:Superfamily: ATP-gated ion channel P2X4 receptor
Query Match 30.5%; Score 679.5; DB 2; Length 397;
Best Local Similarity 42.4%; Pred. No. 2.7e-52;
Matches 146; Conservative 51; Mismatches 122; Indels 25; Gaps 9;
QY 20 WALLAKGYQGRDLEPQPSIIITKLKGVSVTQIKELGNRLMDVADFKPKPGQGVNFFLVTN 79
Db 41 WVFLHEKAYQVRDRTAIESVTVTKVGFQ-----RYANRVMVDSDYVTPQGTSVFVIITK 95
QY 80 FLVTPAQVQGRCPHEPSVPLANCWVDBDCEGEGTHSHGKVTGCQCVFNGTHRTCEI 137
Db 96 IIVTENQMGFCPENEE--KYRCVSDSQGPERPPGG---GILTRGVNYSVSLRTCEI 149
QY 138 NSWCPVESGVVPSRPLLAQAQNFILFIKNTVTFKFNFSKNALETWDPYFKHCERYEPQ 197
Db 150 QGMCCTEVDTV-EMPIMAEANFTIFIKNSIRFPUNFEKGNLLPNLTDKDKRCRHPPE 208
QY 198 FSPYCPVFRIGDLVAKAGCTFEDLALLGSGVIRVHWDCCDLDTGDSGCWPHYSFQ---L 253
Db 209 KAPFCPIELVGDVVKVFAQQQFAKLARTGGVLGKIGVWCDLDKAWDQCIKPYSFTRLDGV 268
QY 254 QEKS-----YNFRATHWHPGVEARTLLKLYGIRFDILVTGQAGKFGILPTAVLTGTG 308
Db 269 SEKSSVSPQYVNFRAKYKYMENGSEYRLLKAFGIRFDVLYVGNAGKFNIIPTIISSVAA 328
QY 309 AAWLGVTTFPCDLLLLYVDREAHFYWRTKYEEAKAP--KATANS 350
Db 329 FTSVGVGVICLDIILLNPLKGDHVKARKFBEVETILKGTAST 372
RESULT 9
I58099
gene P2X3 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58099
R:Lewis, C.; Neidhart, S.; Holy, C.; North, R.A.; Buell, G.; Surprenant, A.
Nature 377, 432-435, 1995
A:Title: Coexpression of P2X2 and P2X3 receptor subunits can account for ATP-gated current
A:Reference number: I58099; MUID:96008545; PMID:7566120
A:Accession: I58099
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-397 <RES>
A:Cross-references: UNIPROT:P49654; EMBL:X91167; NID:g1030064; PIDN:CAA62594.1; PID:g1030
C:Genetics:
C:Gene: P2X3
C:Superfamily: ATP-gated ion channel P2X4 receptor
Query Match 30.5%; Score 679.5; DB 2; Length 397;
Best Local Similarity 42.4%; Pred. No. 2.7e-52;
Matches 146; Conservative 51; Mismatches 122; Indels 25; Gaps 9;
QY 20 WALLAKGYQGRDLEPQPSIIITKLKGVSVTQIKELGNRLMDVADFKPKPGQGVNFFLVTN 79
Db 41 WVFLHEKAYQVRDRTAIESVTVTKVGFQ-----RYANRVMVDSDYVTPQGTSVFVIITK 95
QY 80 FLVTPAQVQGRCPHEPSVPLANCWVDBDCEGEGTHSHGKVTGCQCVFNGTHRTCEI 137
Db 96 MIVTENQMGFCPENEE--KYRCVSDSQGPERPPGG---GILTRGVNYSVSLRTCEI 149

QY 138 WSWCPVSGVPSRPLLAQAQNTFLFKNTVTFSKFNFSKNALETWDPYFKHCRYPFQ 197
Db 150 QGWCPEVDTV-EMPIMAEAFNFTIFKNSIRFPLNFKGNLLNLTDKDIKRCRPHPE 208
QY 198 FSPYCPVFRIGDLVAKAGTFFEDLALGSGVIRVHWCDDLDTGSGCWPVHSPFO----L 253
Db 209 KAPFCPILEGVGVFAGQDFAKLARTGGLGKIGWVCDLDKAWDCIPKYSFTRLDGV 268
QY 254 QSKS-----YNFRATTHWQPGVEARTLLKLYGIRFOILVTGQAGKFLGPIPTAVTLGTG 308
Db 269 SEKSVSPGYNFRFAKYKXGSEYRILLKAFGRFDVLVYGNAGKNFIPTIISVVAA 328
QY 309 AAWLGVVTFPFDLLILLYVDREAHFVYRTKYEBKAP--KATANS 350
Db 329 FTSVGVTGLCDIILLNFKLGADHYKARKFEVETTLKGTAST 372
RESULT 10
B91194
probable enzyme [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
R:Accession: B91194
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B91194
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-562 <HAY>
A:Cross-references: UNIPROT:Q8XD89; GB:BA000007; PIDN:BA037945.1; PID:G13363997; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs4522

Query Match 4.3%; Score 96.5; DB 2; Length 562;
Best Local Similarity 18.6%; Pred. No. 2.1; Indels 104; Mismatches 40; Gaps 9;
Matches 50; Conservative 40; Mismatches 104; Indels 75; Gaps 9;
QY 14 DYKTEKALLAKGYQERDLEPFQFSIITKLKGVSVTQIKELGNRLNDVADFKPPQGENV 73
Db 342 DKXQVRNIGSVRRWQEWDIAPGQDILVSLAQGIPRIDDV--VVRGAERTKPTPPENR 398
QY 74 FFLVNTFLVTPAQVQGRCEHSPVPLANCWVDEDCPEGEGGTHSHGVKTCQCVVENGTHR 133
Db 399 FNSLTCTCFASDV-----CQQFISRLV--WLGSKQVLGLDGIAGEAGWR-----ALHQTHR 446
QY 134 TCEIWSWCPVSGVPSRPLLAQAQNTFLFKNTVTFSKFNFSKNALETWDPYFKHCR 193
Db 447 FEHIFSWLLLTPEQLQNTPGIAKS-----KSAQLWHRFNLARKQPFTRW----- 490
QY 194 YEPQSPYCPVFRIGDLVAKAGTFFEDLALGSGVIRVHWCDDLDTGSGCWPVHSPFOL 253
Db 491 -----VMANGIPLTRAA-----LNASDERSWSQLLFS- 517
QY 254 QSKSYNFRATTHWQPGV---EARTLLK 279
Db 518 -----TEQFWQQLPFGTSGRGRQVIE 538
RESULT 11
C86041
probable enzyme yicF [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
R:Accession: C86041
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C86041
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-562 <STO>
A:Cross-references: UNIPROT:Q8XD89; GB:AE005174; NID:ql2518406; PIDN:AAG58791.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yicF
Query Match 4.3%; Score 96.5; DB 2; Length 562;
Best Local Similarity 18.6%; Pred. No. 2.1; Indels 75; Gaps 9;
Matches 50; Conservative 40; Mismatches 104; Indels 75; Gaps 9;
QY 14 DYKTEKALLAKGYQERDLEPFQFSIITKLKGVSVTQIKELGNRLNDVADFKPPQGENV 73
Db 342 DKXQVRNIGSVRRWQEWDIAPGQDILVSLAQGIPRIDDV--VVRGAERTKPTPPENR 398
QY 74 FFLVNTFLVTPAQVQGRCEHSPVPLANCWVDEDCPEGEGGTHSHGVKTCQCVVENGTHR 133
Db 399 FNSLTCTCFASDV-----CQQFISRLV--WLGSKQVLGLDGIAGEAGWR-----ALHQTHR 446
QY 134 TCEIWSWCPVSGVPSRPLLAQAQNTFLFKNTVTFSKFNFSKNALETWDPYFKHCR 193
Db 447 FEHIFSWLLLTPEQLQNTPGIAKS-----KSAQLWHRFNLARKQPFTRW----- 490
QY 194 YEPQSPYCPVFRIGDLVAKAGTFFEDLALGSGVIRVHWCDDLDTGSGCWPVHSPFOL 253
Db 491 -----VMANGIPLTRAA-----LNASDERSWSQLLFS- 517
QY 254 QSKSYNFRATTHWQPGV---EARTLLK 279
Db 518 -----TEQFWQQLPFGTSGRGRQVIE 538
RESULT 12
T47344
hypothetical protein F18P9.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
A:Accession: T47344
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24458
A:Accession: T47344
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-372 <NYA>
A:Cross-references: UNIPROT:Q9M1L9; EMBL:AL138654
A:Experimental source: cultivar Columbia; BAC clone F18P9
C:Genetics:
A:Map position: 3
A:Introns: 125/3; 194/3
A:Note: F18P9.20
Query Match 4.3%; Score 95; DB 2; Length 372;
Best Local Similarity 21.7%; Pred. No. 1.6;
Matches 73; Conservative 33; Mismatches 110; Indels 120; Gaps 20;
QY 16 KTERKALLAKGYQERDLEPFQFSIITKLKGVSVT-----QIKELGNRLNDVADFKVP--PQ 69
Db 51 KSDQW-----CQSPENP-----ASKRSVAVTTGGFQSRDGGGVAGQDFEKSQPC 98
QY 70 GENVFELVT-NFLVTPAQVQGRCEH-----PSVPLANCW----- 103
Db 99 GVGICLILTNTPKNPKRKYKPNRENGCGFFQWCDAVQSSGTGTTTSSNGXGNDT 158
QY 104 --VDEDCPEGEGGTHSHGVKTCQ-----CVVFNQTHRTCEIWSWCPVSGVPSRPL 153
Db 159 KFPDHCQPCGAGLCRVLTAKTGENVGRQYRCVPFEG---SCGFKWC--NDNVSSPTS 213
QY 154 LAQAQNTFLFKNTVTFSKFNFSKNA-----LETWDPYFKHCRYPQSPYCPV---- 204

Db 214 YGVTKN-----SNFGSDTRGYQNAKTGTFCY--KCKEGHWARDCTVQSDT 258
QY 205 -----FRIG-----DLVAKAG-----GTFEDLALLGG--SVGIRVHM--D 235
Db 259 GPVKSTSAAGDCFKGKPGHNSRDTAGSGPKYEPGQMKSSSSGECYKCGKQHSRD 318
QY 236 CULDRTGDSGCWPHYFQJQKES-----YNFRATFW 266
Db 319 C---TCQSSNQFQSQQAQKSTSTGDCYKCGKAGHW 351
RESULT 13
F71565
probable isoleucine-tRNA ligase (EC 6.1.1.5) - Chlamydia trachomatis (serotype D, strain
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: F71565
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:9900809; PMID:9784136
A:Accession: F71565
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1036 <ARN>
A:Cross-references: UNIPROT:084022; GB:AE001277; GB:AE001273; NID:93328408; PIDN:AA66760
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: ileS
C:Superfamily: isoleucine-tRNA ligase
C:Keywords: ligase
Query Match 4.3%; Score 95; DB 2; Length 1036;
Best Local Similarity 19.8%; Pred. No. 6.1;
Matches 61; Conservative 40; Mismatches 107; Indels 100; Gaps 16;
QY 14 DYKTEKW-ALLAKGYQRDLPEQFSIITKLKGVSVTQIKELGNRLWDVADFKPPQGEN 72
Db 266 DRESYEWIGQLSGKSLVQSYEPFLFPYQDKKELEARILP-----ADFISEGTG 317
QY 73 VFLLTNFLVTPAQVQR-----CPEHSPVPLANCWDEDCPEGEGTHSHGVK--TGQC 125
Db 318 IVHAPAF-----GEADFFACQEH-NVPLV-----CPVDNQGCYTAEVKDFVGEY 361
QY 126 V-----VENGT--HRTCEIWSNCPVESGVVPSRPLLAQAQNFLLIKN 166
Db 362 IKSADKGIARLKNENKLFYQGTVHRVFPFCWR-----TDSPLIYKAVN-SWFFV-- 409
QY 167 TVTESKFNFSKNALETWDTPTPKHCY-----EPQFSYPCVFPFRIGDLVA 212
Db 410 AVEKVKSKWLKANESIIHTPEHIKQGRFGKLEGARDWAISSRYWGTPTPIWSDGGL 469
QY 213 KAGTFEDLALIGGS--VGIRVHWCDDLDGDSG-----CW-----PHY 249
Db 470 LVIGSIQLEALSGQKIVDLRHFIDEIENQNGKSRFRIPYVDFDSCAMPYAQNHY 529
QY 250 SFQLOEKS 257
Db 530 PPERAET 537
RESULT 14
A65166
hypothetical 63.2K protein (gmk 5'region) - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: A65166; S43040; S24191
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A65166
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-562 <BLAN>
A:Cross-references: GB:AE000442; GB:U00096; NID:92367253; PIDN:AA66761.1; PID:91790079;
A:Experimental source: strain K-12, substrain MG1655
R:Gentry, D.; Bengra, C.; Ikehara, K.; Cashel, M.
J. Biol. Chem. 268, 14316-14321, 1993
A:Title: Guanylate kinase of Escherichia coli K-12.
A:Reference number: S43040; MUID:93300828; PMID:8390989
A:Accession: S43040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 2-218 <GEN>
A:Cross-references: EMBL:M84400
C:Genetics:
A:Gene: yicF
Query Match 4.2%; Score 94.5; DB 2; Length 562;
Best Local Similarity 18.6%; Pred. No. 3.1; Mismatches 40; Indels 75; Gaps 9;
Matches 50; Conservative 40; Mismatches 40; Indels 75; Gaps 9;
QY 14 DYKTEKWALLAKGYQERDLPEQFSIITKLKGVSVTQIKELGNRLWDVADFKPPQGENV 73
Db 342 DKKVQRVNI-GSVRRQCEWDIAPGQDQILVSLAGQIPRIDDV---VVRGAERTKTPPENR 398
QY 74 FELVTNFLTTPAQVQRCPEHSPVPLANCWDEDCPEGEGTHSHGVKTCQCVWENGTHR 133
Db 399 FNSLTCYFASDV-----COEQFISRLV--WLGAKQVLGLDGTGEAGWR-----ALHQTHR 446
QY 134 TCEIWSNCPVESGVVPSRPLLAQAQNFLLIKNTVTFKFNFSKNALETWDTPTFKHCR 193
Db 447 FEHIFSWLLTPEQLQNTFGIAKS-----KSAQLWHQFNLRKQPFTRW-----490
QY 194 YBPQFSYPCVFPFRIGDLVAKAGTFEDLALIGSGVIRVHWCDDLDGDSGCWPHYSQL 253
Db 491 -----VVMANGIPLTRAA-----LNASDRSWSQLLFS- 517
QY 254 QEKSYNFRATHWQEPGV---EARTLLK 279
Db 518 -----TEQFWQQLPGTSGRARQVIE 538
RESULT 15
I38000
Lutheran blood group glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38000; S51663
R:Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, W.J.;
Proc. Natl. Acad. Sci. U.S.A. 92, 5496-5500, 1995
A:Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin supe
A:Reference number: I38000; MUID:95296337; PMID:7777537
A:Accession: I38000
A:Molecule type: mRNA
A:Residues: 1-628 <RES>
A:Cross-references: UNIPROT:P50895; EMBL:X83425; NID:9603559; PIDN:CAA58449.1; PID:960356
A:Note: parts of this sequence, including the amino end of the mature form, were confirme
C:Genetics:
A:Gene: GDB:LU
A:Cross-references: GDB:120155; OMIM:111200
A:Map position: 19q12-19q13
C:Keywords: glycoprotein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-628/Product: Lutheran blood group glycoprotein #status experimental <MAT>
Query Match 4.2%; Score 94.5; DB 2; Length 628;
Best Local Similarity 20.8%; Pred. No. 3.6; Mismatches 136; Indels 113; Gaps 17;
Matches 76; Conservative 41; Mismatches 41; Indels 113; Gaps 17;
QY 1 MGSPGATTGW-----GLL-----DYKTEKWALLAKGYQERDLPEQFSIITKLKGVSVT 49
Db 271 VGSPTPGACWVRREGDTVQLCRGDSGSPSEVTLFLRQDEQEVNLNLEGNLTLEGVTRG 330

Search completed: November 21, 2004, 15:04:20
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2004, 15:00:26 ; Search time 144 Seconds
(without alignments)
995.984 Million cell updates/sec

Title: US-09-820-095B-2

Perfect score: 2226

Sequence: 1 MGSPATTGGLLDYKTEKW.....TPGWPCSSDTHLPTHSGSL 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2226	100.0	405	10	US-09-820-095-2
2	2203	99.0	431	10	US-09-820-095-4
3	1080.5	48.5	364	15	US-10-051-874-125
4	825.5	37.1	422	17	US-10-128-558-144
5	816	36.7	388	9	US-09-833-082-2
6	816	36.7	388	15	US-10-455-552-2
7	810	36.4	388	15	US-10-386-414-17
8	744	33.4	399	14	US-10-352-684A-54
9	709	31.9	459	14	US-10-345-680-11
10	709	31.9	459	15	US-10-051-874-123
11	704.5	31.6	397	16	US-10-408-765A-2202
12	694	31.2	402	11	US-09-764-875-905
13	694	31.2	404	15	US-10-051-874-124

14	693	31.1	497	15	US-10-051-874-120	Sequence 120, App
15	673.5	30.3	287	15	US-10-455-552-3	Sequence 3, Appl1
16	631	28.3	347	15	US-10-051-874-121	Sequence 121, App
17	631	28.3	447	15	US-10-051-874-122	Sequence 122, App
18	615	27.6	473	15	US-10-051-874-42	Sequence 42, Appl
19	611.5	27.5	595	16	US-10-408-765A-2166	Sequence 2166, Ap
20	608.5	27.3	595	16	US-10-622-313-1	Sequence 1, Appl1
21	608.5	27.3	595	16	US-10-789-241-40	Sequence 40, Appl1
22	606.5	27.2	595	10	US-09-977-221-4	Sequence 4, Appl1
23	606.5	27.2	595	16	US-10-766-978-4	Sequence 4, Appl1
24	583	26.2	348	15	US-10-336-472-52	Sequence 52, Appl1
25	545.5	24.5	274	15	US-10-336-472-54	Sequence 54, Appl1
26	500	22.5	260	14	US-10-104-047-2151	Sequence 2151, Ap
27	379.5	17.0	280	9	US-09-764-847-739	Sequence 739, App
28	379.5	17.0	280	11	US-09-764-875-1131	Sequence 1181, Ap
29	373.5	17.0	280	14	US-10-092-154-739	Sequence 739, App
30	250	11.2	50	9	US-09-864-761-38753	Sequence 38753, A
31	206	9.3	46	9	US-09-864-761-35496	Sequence 35496, A
32	102	4.6	636	14	US-10-156-761-13432	Sequence 13432, A
33	98.5	4.4	442	15	US-10-425-114-58714	Sequence 58714, A
34	98.5	4.4	450	17	US-10-425-115-346201	Sequence 346201, A
35	98.5	4.4	3564	15	US-10-016-248-45	Sequence 45, Appl1
36	95	4.3	754	15	US-10-108-260A-4450	Sequence 4450, Ap
37	94.5	4.2	394	9	US-09-925-301-1388	Sequence 1388, Ap
38	94.5	4.2	394	15	US-10-264-049-3011	Sequence 3011, App
39	94.5	4.2	628	14	US-10-176-847-108	Sequence 108, App
40	94.5	4.2	628	14	US-10-205-823-246	Sequence 246, App
41	94.5	4.2	628	14	US-10-257-021-6	Sequence 6, Appl1
42	94.5	4.2	628	14	US-10-257-021-70	Sequence 70, Appl1
43	94	4.2	1000	10	US-09-823-187-6	Sequence 6, Appl1
44	93.5	4.2	595	15	US-10-276-774-2369	Sequence 2369, Ap
45	93.5	4.2	2669	15	US-10-016-248-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1

US-09-820-095-2
; Sequence 2, Application US/09820095
; Publication No. US20030233668A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001202
; CURRENT APPLICATION NUMBER: US/09/820,095
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-09-820-095-2

Query Match 100.0%; Score 2226; DB 10; Length 405;
Best Local Similarity 100.0%; Pred. No. 9.3e-214;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSPATTGGLLDYKTEKWALLAKKGYQERDLEPOFSITKLKGVSVTOIKELGNLWD	60
Db	1	MGSPATTGGLLDYKTEKWALLAKKGYQERDLEPOFSITKLKGVSVTOIKELGNLWD	60
Qy	61	VADPVKPPQGENVFFLTNLFVTPAQVQGRCPHPSVPLANCWVDEDCPEGGTHSHGV	120
Db	61	VADPVKPPQGENVFFLTNLFVTPAQVQGRCPHPSVPLANCWVDEDCPEGGTHSHGV	120
Qy	121	KTGCVVFNHTRTCEIWSWCPVSGVVPSPRLLAQONFTLPIKNTVTSKFNFSKNA	180
Db	121	KTGCVVFNHTRTCEIWSWCPVSGVVPSPRLLAQONFTLPIKNTVTSKFNFSKNA	180

181 LETWDPYFKHCRVYQPSYCPVPRIGDLVAKAGGTFFEDLALLGGSGVIRVHWDCLDT 240
Db 181 LETWDPYFKHCRVYQPSYCPVPRIGDLVAKAGGTFFEDLALLGGSGVIRVHWDCLDT 240
QY 241 GDSGCWPHYSFOLQSKSYNFRATATWHPQGVARTLLKLYGIRFDILVTQAGKFGILP 300
Db 241 GDSGCWPHYSFOLQSKSYNFRATATWHPQGVARTLLKLYGIRFDILVTQAGKFGILP 300
QY 301 TAVTLGTGAAMLVGVTFFCDLLLVVDREAHFYRTKYEBEAKAPKATANSVWRELALASQ 360
Db 301 TAVTLGTGAAMLVGVTFFCDLLLVVDREAHFYRTKYEBEAKAPKATANSVWRELALASQ 360
QY 361 ARLAELRRSSAPATAAGSQTQTPGWPCCPSDTHLPTHSGSL 405
Db 361 ARLAELRRSSAPATAAGSQTQTPGWPCCPSDTHLPTHSGSL 405
RESULT 2
US-09-820-095-4
; Sequence 4, Application US/09820095
; Publication No. US20030233668A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001202
; CURRENT APPLICATION NUMBER: US/09/820,095
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Human
US-09-820-095-4

Query Match 99.0%; Score 2203; DB 10; Length 431;
Best Local Similarity 94.0%; Fred. No. 2e-211;
Matches 405; Conservative 0; Mismatches 0; Indels 26; Gaps 1;
QY 1 MGSPGATTGWLGLDYKTEK-----WALLAKKGQERDLE 34
Db 1 MGSPGATTGWLGLDYKTEKYWTRNRYGALQRLIQFGIVVVVGVWALLAKKGQERDLE 60
QY 35 POFSIITKLKGVSTQIKELGNRLMDVADFKPPQGVNFVFLVTFNLTQAGKFGILP 94
Db 61 POFSIITKLKGVSTQIKELGNRLMDVADFKPPQGVNFVFLVTFNLTQAGKFGILP 120
QY 95 PSVPLANCWVDEDCPEGGGTHSHGVKTGCQVFNHGTCTCEIWSWCPVSGVPSRPL 154
Db 121 PSVPLANCWVDEDCPEGGGTHSHGVKTGCQVFNHGTCTCEIWSWCPVSGVPSRPL 180
QY 155 AQAQNTLFIKNTVTSKFNFSKNALETWDPYFKHCRVYQPSYCPVPRIGDLVAKA 214
Db 181 AQAQNTLFIKNTVTSKFNFSKNALETWDPYFKHCRVYQPSYCPVPRIGDLVAKA 240
QY 215 GGTFFEDLALLGGSGVIRVHWDCLDTGDSGCWPHYSFOLQSKSYNFRATATWHPQGV 274
Db 241 GGTFFEDLALLGGSGVIRVHWDCLDTGDSGCWPHYSFOLQSKSYNFRATATWHPQGV 300
QY 275 RTLLKLYGIRFDILVTQAGKFGILPTAVTLGTGAAMLVGVTFFCDLLLVVDREAHFY 334
Db 301 RTLLKLYGIRFDILVTQAGKFGILPTAVTLGTGAAMLVGVTFFCDLLLVVDREAHFY 360
QY 335 RTKYEBEAKAPKATANSVWRELALASQARLAELRRSSAPATAAGSQTQTPGWPCCPS 394
Db 361 RTKYEBEAKAPKATANSVWRELALASQARLAELRRSSAPATAAGSQTQTPGWPCCPS 420
QY 395 DTHLPTHSGSL 405
Db 421 DTHLPTHSGSL 431

RESULT 3
US-10-051-874-125
; Sequence 125, Application US/10051874
; Publication No. US20040005557A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Alsobrook II, John P
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Boldog, Ferenc AM
; APPLICANT: Vernet, Corine AM
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Casman, Stacie J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Pena, Carol EA
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Millet, Isabelle
; APPLICANT: Miller, Charles E
; APPLICANT: Lepley, Denise M
; APPLICANT: Smithson, Glennda
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Herrman, John L
; APPLICANT: Peyman, John A
; APPLICANT: Gorman, Linda
; APPLICANT: Mezes, Peter D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William M
; APPLICANT: Liu, Xiaohong
; APPLICANT: Ellerman, Karen
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 21402-245
; CURRENT APPLICATION NUMBER: US/10/051,874
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/268,595
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/325,306
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/262,587
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/272,409
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/262,454
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/276,777
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/291,672
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/330,336
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/265,530
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/261,376
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Artificial Sequence

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/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: P2X_receptor
/ OTHER INFORMATION: domain sequence
US-10-051-874-125

Query Match      48.5%; Score 1080.5; DB 15; Length 364;
Best Local Similarity 56.1%; Pred. No. 4.1e-99;
Matches 203; Conservative 44; Mismatches 80; Indels 35; Gaps 4;

QY 14 DYKTEK-----WALLAKKGQERDLEPOFSIITKLKGV 47
Db 2 DYKTPKVVVRNKKVGLLNRLVQLLLVYVGVWFLEKGYQDSOTSLQSSVITKVGVA 61

QY 48 VTOIKELGNRLMDVADFVKPPQGENVFFLVNPLVTPAQVQGRCPHPSPVLANCWDED 107
Db 62 VNTSELGNRVMDVADYVIPPQGENVFFVVTNPIVTPNQTQCTCEHPPEVPDGTCKSDSD 121

QY 108 CPEGEGTHSHGVKTCQCVVNGT-HRTCEIWSWCPVBSGVPSPLLAQAQNFILTKN 166
Db 122 CTAGEAGTHNGIKTGRCVAFNGSVRTCEIFAWCPVEVDTPFNPLLKEAENFTIFKN 181

QY 167 TVTFSKFNFSKNALETWPTVFKHCRYEPQSPYCPVFRIGDLVAKAGTFEDLALGG 226
Db 182 SIRFPKFNFSKGNLLENKTDLYLKHCRPHPTNDPYCPIFRLDGVVEKAGQDFQDLAKGG 241

QY 227 SVGIRVHWDCLDTCGSCWPHYSFO----LQES-----YNFRTHHWEOQGVARTLL 278
Db 242 VIGLIINWDCDDKAASECNPHYSFRRLDNKKEKSVSPGYNFRFAKYRDNNNGVEYRLL 301

QY 279 KLYGIRFDILVTQAGKFGILPTAVTLGTGAWLGVWTFECLLLLYVDREAHFYWRKY 338
Db 302 KAYGIRFDVLNGKAGKFPDIITINIGSLASLGVLGFLCDLLILLYLKKHFYRDKKF 361

QY 339 EE 340
Db 362 EE 363

RESULT 4
US-10-128-558-144
/ Sequence 144, Application US/10128558
/ Publication No. US20040219521A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Weng, Gezhi
/ APPLICANT: Boyle, Bryan J
/ APPLICANT: Drmanac, Radoje T
/ TITLE OF INVENTION: Novel Nucleic Acids and
/ FILE REFERENCE: Polypeptides
/ CURRENT APPLICATION NUMBER: US/10128,558
/ PRIOR FILING DATE: 2002-04-22
/ PRIOR APPLICATION NUMBER: US 60/339,453
/ PRIOR FILING DATE: 2001-12-11
/ PRIOR APPLICATION NUMBER: US 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: PCT/US00/35017
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: PCT/US01/03800
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: US 09/515,126
/ PRIOR FILING DATE: 2000-02-28
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/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 412
/ SOFTWARE: DC_FL_Genes Version 6.0
/ SEQ ID NO 144
/ LENGTH: 422
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-128-558-144

Query Match      37.1%; Score 825.5; DB 17; Length 422;
Best Local Similarity 42.7%; Pred. No. 1.7e-73;
Matches 166; Conservative 63; Mismatches 125; Indels 35; Gaps 7;

QY 20 WALLAKKGQERDLEPOFSIITKLKGVSVTQIKELGNRLMDVADFVKPPQGENVFFLVN 79
Db 46 WVFWEKGYQETD-SVVSSTTKVGVAVNTSKLGFRIWDVADYVIPAQENSLSFVMTN 104

QY 80 FLVTPAQVQGRCPHPSPVLANCWDEDCEGEGTHSHGVKTCQCVVNGTHRTCEIWS 139
Db 105 VILTMNQTQGLCPPIPDATTV-CKSDASCTAGSAGTHSNVSTGRCVAFNGSVKTCVAA 163

QY 140 WCPVESGV-VPSRPELLAQONFTLFIKNTVTFESKFNESKNALETWPTVFKHCRYEPOF 198
Db 164 WCPVEDDTHVPQAPAFKAAENFLLVKNNTWYKFNESKNNILPNTITTYLKSCIYDAKT 223

QY 199 SPYCPVFRIGDLVAKAGTFEDLALGSGVGRVHWDCLDTCGSCWPHYSFQLE--- 255
Db 224 DPFCEPIFRLGKIVENAGHSQDMAVEGGIMGIQVNMDCNLDRAASLCLPRYSFRRLDTRD 283

QY 256 -----KSNFRTHHWEOQGVARTLLKLYGIRFDILVTQAGKFGILPTAVTLGTGA 309
Db 284 VEHNVSGYFRFAKYRDLAGNEQRTLIKAYGIRFDIIVFGKAGKFPDIITMINIGSL 343

QY 310 AWLGWTFECLLLLYVDREAHFYWRKYBEAKAPKATANSVWRELALASQARLAECRLR 369
Db 344 ALLGMATVLCDDIIVLYCMKKELYYREKKYKVVEDYEQVGPS-W----- 385

QY 370 SSAPAPTATAA---GSQTQTPGWPCPSSD 395
Db 386 --PPAGTGLSSLGCGSPGRGPMVGGPSAE 412

RESULT 5
US-09-833-082-2
/ Sequence 2, Application US/09833082
/ Patent No. US20020151480A1
/ GENERAL INFORMATION:
/ APPLICANT: Chun, Miyoung
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ FILE REFERENCE: CARDIOVASCULAR DISEASE USING 10218
/ CURRENT APPLICATION NUMBER: US/09/833,082
/ CURRENT FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 388
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-833-082-2

Query Match      36.7%; Score 816; DB 9; Length 388;
Best Local Similarity 47.0%; Pred. No. 1.4e-72;
Matches 155; Conservative 56; Mismatches 107; Indels 12; Gaps 4;

QY 20 WALLAKKGQERDLEPOFSIITKLKGVSVTQIKELGNRLMDVADFVKPPQGENVFFLVN 79
Db 46 WVFWEKGYQETD-SVVSSTTKVGVAVNTSKLGFRIWDVADYVIPAQENSLSFVMTN 104

QY 80 FLVTPAQVQGRCPHPSPVLANCWDEDCEGEGTHSHGVKTCQCVVNGTHRTCEIWS 139
Db 105 VILTMNQTQGLCPPIPDATTV-CKSDASCTAGSAGTHSNVSTGRCVAFNGSVKTCVAA 163
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QY 140 WCPVBSGV-VPSRPLLAQAQNTFLIKNTVTFSKFNKSNALETWDPYFKHCYEPQF 198
 DB 164 WCPVEDDTHVPQAPFLKAAENFTLLVKNINWPKFNFSKRNILPNTITTYLKSICYDAKT 223
 QY 199 SPYCPVFRIGDLVAKAGTFEDLALLGGVGRVHWDCLDLDGSGCWPHYSFQLOE--- 255
 DB 224 DFCPIFRGLKIVENAGHSFQDMAVEGGIMGIQVNDONLDRASLCLPRYSFRFLDTRD 283
 QY 256 -----KSNFRATTHWEPQVEARTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGA 309
 DB 284 VEHNVSPGYNFRFAKYRDLAGNEORTLIKAYGIRFDIIVFGKAGKFDIIPMTINIGSGL 343
 QY 310 AWLGWVTFCDLLLYVDREAHFYWRKYE 339
 DB 344 ALLGMATVLCDIIVLYCMKRLIYREKKYK 373

RESULT 6
 US-10-455-552-2
 ; Sequence 2, Application US/10455552
 ; Publication No. US20040018533A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Adam, Gail Isabel
 ; APPLICANT: Langdown, Maria
 ; APPLICANT: Roth, Richard
 ; APPLICANT: Denissenko, Mikhail
 ; APPLICANT: Smylie, Kevin
 ; TITLE OF INVENTION: DIAGNOSING PREDISPOSITION TO FAT
 ; TITLE OF INVENTION: DEPOSITION AND THERAPEUTIC METHODS FOR REDUCING FAT
 ; TITLE OF INVENTION: DEPOSITION AND TREATMENT OF ASSOCIATED CONDITIONS
 ; FILE REFERENCE: 52459-20030.00
 ; CURRENT APPLICATION NUMBER: US/10/455,552
 ; CURRENT FILING DATE: 2003-06-04
 ; PRIOR APPLICATION NUMBER: US 60/386,012
 ; PRIOR FILING DATE: 2002-06-04
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 388
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-455-552-2

Query Match 36.7%; Score 816; DB 15; Length 388;
 Best Local Similarity 47.0%; Pred. No. 1.4e-72;
 Matches 155; Conservative 56; Mismatches 107; Indels 12; Gaps 4;
 QY 20 WALLAKKGQERDLEPQFSIITKLKGVSVTQIKELGNRLWDVADVPKPPQGENVFLVTN 79
 DB 46 WYFVWKEGQETD-SVSVSVTTKVGAVTNTSKLGRINDVADYVIPAEENSLFVMTN 104
 QY 80 FLVTPAQVQGRCPHPSVPLANCWVDEDCPEGEGTHSHGVKTGCQVVFNGTHRTCEIWS 139
 DB 105 VILTMNQTOGLCPEDATTV-CKSDASCTAGSAGTHSGVSTGRCAVFNAGSVKTCVAA 163
 QY 140 WCPVBSGV-VPSRPLLAQAQNTFLIKNTVTFSKFNKSNALETWDPYFKHCYEPQF 198
 DB 164 WCPVEDDTHVPQAPFLKAAENFTLLVKNINWPKFNFSKRNILPNTITTYLKSICYDAKT 223
 QY 199 SPYCPVFRIGDLVAKAGTFEDLALLGGVGRVHWDCLDLDGSGCWPHYSFQLOE--- 255
 DB 224 DFCPIFRGLKIVENAGHSFQDMAVEGGIMGIQVNDONLDRASLCLPRYSFRFLDTRD 283
 QY 256 -----KSNFRATTHWEPQVEARTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGA 309
 DB 284 VEHNVSPGYNFRFAKYRDLAGNEORTLIKAYGIRFDIIVFGKAGKFDIIPMTINIGSGL 343
 QY 310 AWLGWVTFCDLLLYVDREAHFYWRKYE 339
 DB 344 ALLGMATVLCDIIVLYCMKRLIYREKKYK 373

RESULT 7

US-10-386-414-17
 ; Sequence 17, Application US/10386414
 ; Publication No. US20040006016A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; APPLICANT: Robison, Keith E.
 ; APPLICANT: White, David
 ; APPLICANT: Williamson, Mark W.
 ; APPLICANT: Cook, William James
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: Macbeth, Kyle J.
 ; APPLICANT: Carroll, Joseph M.
 ; APPLICANT: Chun, Miyoung
 ; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
 ; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MPI03-0210WNIM
 ; CURRENT APPLICATION NUMBER: US/10/386,414
 ; CURRENT FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: 09/426,282
 ; PRIOR FILING DATE: 1999-10-25
 ; PRIOR APPLICATION NUMBER: 09/668,266
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 09/330,970
 ; PRIOR FILING DATE: 1999-06-11
 ; PRIOR APPLICATION NUMBER: 09/724,599
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/860,193
 ; PRIOR FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 10/283,023
 ; PRIOR FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: 60/335,044
 ; PRIOR FILING DATE: 2001-10-31
 ; PRIOR APPLICATION NUMBER: 10/010,943
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: 60/254,037
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: 09/833,082
 ; PRIOR FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 388
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(388)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-10-386-414-17

Query Match 36.4%; Score 810; DB 15; Length 388;
 Best Local Similarity 46.7%; Pred. No. 5.4e-72;
 Matches 154; Conservative 56; Mismatches 108; Indels 12; Gaps 4;
 QY 20 WALLAKKGQERDLEPQFSIITKLKGVSVTQIKELGNRLWDVADVPKPPQGENVFLVTN 79
 DB 46 WYFVWKEGQETD-SVSVSVTTKVGAVTNTSKLGRINDVADYVIPAEENSLFVMTN 104
 QY 80 FLVTPAQVQGRCPHPSVPLANCWVDEDCPEGEGTHSHGVKTGCQVVFNGTHRTCEIWS 139
 DB 105 VILTMNQTOGLCPEDATTV-CKSDASCTAGSAGTHSGVSTGRCAVFNAGSVKTCVAA 163
 QY 140 WCPVBSGV-VPSRPLLAQAQNTFLIKNTVTFSKFNKSNALETWDPYFKHCYEPQF 198
 DB 164 WCPVEDDTHVPQAPFLKAAENFTLLVKNINWPKFNFSKRNILPNTITTYLKSICYDAKT 223
 QY 199 SPYCPVFRIGDLVAKAGTFEDLALLGGVGRVHWDCLDLDGSGCWPHYSFQLOE--- 255
 DB 224 DFCPIFRGLKIVENAGHSFQDMAVEGGIMGIQVNDONLDRASLCLPRYSFRFLDTRD 283
 QY 256 -----KSNFRATTHWEPQVEARTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGA 309
 DB 284 VEHNVSPGYNFRFAKYRDLAGNEORTLIKAYGIRFDIIVFGKAGKFDIIPMTINIGSGL 343

[illegible]


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; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2202
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2202

Query Match      31.6%; Score 704.5; DB 16; Length 397;
Best Local Similarity 36.4%; Pred. No. 2.1e-61;
Matches 156; Conservative 59; Mismatches 114; Indels 101; Gaps 11;

QY 12 LLDYKTEK-----WALLAKGYQERDLSPQSIITKLG 45
Db 13 LFDYKTEKVIANKKKVGLLYRLLOASILAYLVVWFLIKGQVDVTSLSQSAVITKVG 72

QY 46 VSVTOIKELNRLNLDVADFKPPQGENVFELVTNFLTPTAQVQRCRPEHPSVPLANCWD 105
Db 73 VAFNTNSDLGORLDVADVYVIPAQNE-----GIPDGACSKD 108

QY 106 EDCPEGEGGTHSGVTKGCV-VFNGTHTTCEIWSWCPVBSGVVPSRPLLAQAQNFPT 164
Db 109 SDCHAGEAVTAGVGTGRCLRENLAGTCEIFAWCPLTSSRPEEPFLKEADFTIFI 168

QY 165 KNTVTSKFNFKSNALETWDPYFKHCRVPEQSPYCPVFRIGDLVAKAGGTEDL 224
Db 169 KHIRFPKENFS-NVMDVKDRSFLKSCFGRK-NHYCFIRLGSVIRWAGSDFQDIALE 226

QY 225 GSGVIRVHWDCDLDTGDSGCWPHYSF-QLOEK-----SYNFRATATHWQPGVEART 276
Db 227 GGIVGINIEWNCDLDAASECHPHYSFSLDNKLSKSVSSGYNFRFARYRDAAGVEFRT 286

QY 277 LLKLYGIRDLVTGQAGKFLIPTAVTLTGTAAMLVGVTFECDDLILLYVDEAHFYWT 336
Db 287 LMKVYGIIRDVWVNGK-----AFFCDLVLIVLIKKRREFYRDK 324

QY 337 KYEAKAPKATANSVWRELASQARLAECRLRSAPA-----PTATAAGSQ 383
Db 325 KYEEVRGLDSSQEADE--ASGLGLSEQL--TSGPGLLGMPEQELQEPPEAKRGSS 379

QY 384 TQTPGWPCP 392
Db 380 QKNGSVCP 388

RESULT 12
US-09-764-875-905
; Sequence 905, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ202
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 905
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-875-905

Query Match      31.2%; Score 694; DB 11; Length 402;
Best Local Similarity 38.8%; Pred. No. 2.4e-60;
Matches 142; Conservative 63; Mismatches 119; Indels 42; Gaps 7;

QY 10 WCLL-DYKTEK-----WALLAKGYQERDLSPQSIITK 42
Db 20 WSAWDYETPKVIVVVRNRLGLVYRAVQLLILLYFVWVYVFOKSYQSSRGPSIITK 79

QY 43 LKGVSVTQIKELGNLWDVADVPKPPQGENVFELVTNFLTPTAQVQRCRPEHPSVPLANC 102
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RESULT 13

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US-10-051-874-124
; Sequence 124, Application US/10051874
; Publication No. US2004000557A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Alsobrook II, John P
; APPLICANT: Coleman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Boldog, Ferenc
; APPLICANT: Vernet, Corine AM
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Casman, Stacie J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Pera, Carol EA
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Millet, Isabelle
; APPLICANT: Miller, Charles E
; APPLICANT: Lepley, Denise M
; APPLICANT: Smithson, Glenda
; APPLICANT: Baumgarther, Jason C
; APPLICANT: Herrman, John L
; APPLICANT: Peyman, John A
; APPLICANT: Gorman, Linda
; APPLICANT: Mezes, Peter D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William M
; APPLICANT: Liu, Xiaohong
; APPLICANT: Ellerman, Karen
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; FILE REFERENCE: 21402-245
; CURRENT FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/325,306
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US/10/051,874

60/368,595

60/325,306

; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/262,587
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/272,409
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/262,454
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/276,777
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/291,672
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/330,336
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/265,530
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/261,376
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 124
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-051-874-124

Query Match 31.2%; Score 694; DB 15; Length 404;
Best Local Similarity 38.8%; Pred. No. 2.4e-60;
Matches 142; Conservative 63; Mismatches 119; Indels 42; Gaps 7;

Qy 10 WGLL-DYKTEK-----WALLAKGYQERDLEPQFSIITK 42
Db 22 WSALWDYETPKVIIVNRRLGLVYRAVOLLILLFVWVIVFVQKSYQSESGPSSIIITK 81
Qy 43 LKGVSVTQIKELGNRLWDVADFKPQGNVFLVFNFLVTPAQVQGRCPHPSVPLANC 102
Db 82 VKGITTS-----HKVMDVEEVKPEGGSVFSIIITRVEATHSQTQGTCPESIRVHNATC 136
Qy 103 WYDECPGEGGTHSHGVKTGCQV-VENGTHRTCEIWSWCVPESGVPSRPLLAQAQNT 161
Db 137 LSDADCVAGELMNLGNLRTGTCVPIYQYQPSKTCVFGWCVPEDGASVQSLGTWAFNFT 196
Qy 162 LPIKNTVTFKFNFSKNALETWDTYFKHCRIYEPQFSPYCFVFRIGDLVAKAGTFEDL 221
Db 197 ILIKNSIHKPFHFSKGNIAERTD-GYLKRCCTFHEASLDYCPFKLGFIVEKAGESFTEL 255
Qy 222 ALLGSVGRVWDCDLDGDSGCWPHYSFQLOE-----KSNFRATHTHWQPGVEA 274
Db 256 AHKGGVIGVIINWDCDLDLPASECNPKYSFRRLDPKHVPASSGYNFRFA-KYIKINGTTT 314
Qy 275 RTLLKLYGIRFIVLTGQAKGFLIPTAVTLGTGAALGVTFFCDLLLLYVDREAHFYW 334
Db 315 RFLIKAYGIRIDIVHVGQAGKSLIPTIINLATLTSVGVGSLCDWILLTFMKNKYVS 374
Qy 335 RTKYE 340
Db 375 HKKFDK 380

RESULT 14
US-10-051-874-120
; Sequence 120, Application US/10051874
; Publication No. US2004000557A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Alsbrook II, John P
; APPLICANT: Coleman, Steven D
; APPLICANT: Spytex, Kimberly A
; APPLICANT: Boldog, Ferenc
; APPLICANT: Vernet, Corine AM
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Casman, Stacie J
; APPLICANT: Guo, Xiaojia Sasha

; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Pena, Carol EA
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Millet, Isabelle
; APPLICANT: Miller, Charles E
; APPLICANT: Lepley, Denise M
; APPLICANT: Smithson, Glennda
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Herrman, John L
; APPLICANT: Feyman, John A
; APPLICANT: Gorman, Linda
; APPLICANT: Mezes, Peter D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William M
; APPLICANT: Liu, Xiaohong
; APPLICANT: Ellerman, Karen
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 21402-245
; CURRENT APPLICATION NUMBER: US/10/051,874
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/268,595
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/325,306
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/262,587
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/272,409
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/262,454
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/276,777
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/291,672
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/330,336
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/265,530
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/261,376
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 120
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-051-874-120

Query Match 31.1%; Score 693; DB 15; Length 497;
Best Local Similarity 35.0%; Pred. No. 4e-60;
Matches 159; Conservative 66; Mismatches 153; Indels 76; Gaps 10;

Qy 10 WGLL-DYKTEK-----WALLAKGYQERDLEPQFSIITK 42
Db 22 WSALWDYETPKVIIVNRRLGLVYRAVOLLILLFVWVIVFVQKSYQSESGPSSIIITK 81
Qy 43 LKGVSVTQIKELGNRLWDVADFKPQGNVFLVFNFLVTPAQVQGRCPHPSVPLANC 102
Db 82 VKGITTS-----HKVMDVEEVKPEGGSVFSIIITRVEATHSQTQGTCPESIRVHNATC 136
Qy 103 WYDECPGEGGTHSHGVKTGCQV-VENGTHRTCEIWSWCVPESGVPSRPLLAQAQNT 161

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Job time : 146 secs

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Db 137 LSDADCVAGELDMGLNGLRTGRCVPYVQGSFKTCEVFGWCPVEDGASVSQFLGTWAPNET 196
QY 162 LFTKNTVTSKFNFSKNALETWDPYFKHCRVEPOFSYCPVFRIGDLVAKAGTFFDL 221
Db 197 ILKNSIHVPKPHFSKGNADRTD-GYLKRCFPHASDLYCFPKLGFIVEKAGESFTL 255
QY 222 ALLGSGVIRVHWDCCDLDTGSCWPHYSFQLOE-----KSYNERTATHWEOQGVFA 274
Db 256 AHKGGVIGVIINWDCDLDPASECNPKYFRRLDPKHVPASSGYNFRPA-KYIKINGTTT 314
QY 275 RTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGAAGLVW----- 315
Db 315 RTLIKAYGIRIDIVHGOAGKFSLIPTIINLATITSVGVWRNPLWPGSGCGSTRPLHT 374
QY 316 -----TFFCDLLLYVDREAHFYWRTKYEEAKAPKATANSWRELALASQARLAECUR 368
Db 375 GLCWPGSFLCDWILLTFMNKKNVSHKFKDVCPTSPHSGSNPVTLARVLGOAPPEPGH 434
QY 369 RS--SAPAPTATAAGSQ-----TQTPGWPCPSS 394
Db 435 RSEDQHPSPPSGQGQGAECGPAFPPLRCPIS 468

RESULT 15
US-10-455-552-3
; Sequence 3, Application US/10455552
; Publication No. US20040018533A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Gail Isabel
; APPLICANT: Langdown, Maria
; APPLICANT: Roth, Richard
; APPLICANT: Denissenko, Mikhail
; APPLICANT: Smylie, Kevin
; TITLE OF INVENTION: DIAGNOSING PREDISPOSITION TO FAT
; TITLE OF INVENTION: DEPOSITION AND THERAPEUTIC METHODS FOR REDUCING FAT
; TITLE OF INVENTION: DEPOSITION AND TREATMENT OF ASSOCIATED CONDITIONS
; FILE REFERENCE: 52459-20030.00
; CURRENT APPLICATION NUMBER: US/10/455,552
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: US 60/386,012
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-455-552-3

Query Match 30.3%; Score 673.5; DB 15; Length 287;
Best Local Similarity 46.2%; Pred. No. 1.7e-58;
Matches 126; Conservative 47; Mismatches 89; Indels 11; Gaps 3;

QY 77 VTNFLTQAQVQGRCPHPSVPLANCWVDEDCPEGEGGTHSGVKTGCVVFNHRTCE 136
Db 1 MTNVILTNQTLQGLPEIPDATTV-CKSDASCTAGSAGTHSNGVSTGRCAVFNHRTCE 59
QY 137 INSWCPVPSGV-VPSRPLLAQONTLFIKNTVTSKFNFSKNALETWDPYFKHCKYE 195
Db 60 VAAWCPVEDDTHVQPAFLKAAENFTLLVKNINWPKFNFSKRNILPNITTYLKSCTYD 119
QY 196 POFSPYCPVERIGDLVAKAGTFFDLALLGSGVIRVHWDCCDLDTGDSGWPHYSFQLOE 255
Db 120 AKTDPCFIFRLGKIVEAGHSFQMAVEGGIMGQVNWDCNDRASLCPLRYSFRRLD 179
QY 256 -----KSYNERTATHWEOQGVFA 339
Db 180 TRDVEHNVSPGYNFRFAKYRDLAGNEQRTLIKAYGIRFDILVTGQAGKFGLIPTAVTLG 306
QY 307 TGAWLGVVTFPCDLLLYVDREAHFYWRTKYE 339
Db 240 SGLALLGNATVLCDIIVLYCMKKRLRYREKKYK 272
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OM protein - protein search, using sw model

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Title: US-09-820-095B-2
Perfect score: 2226
Sequence: 1 MGSPGATTGGLLDYKTEK.....TFGWPCPSDTHLPHSGSL 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2203	99.0	431	3	US-09-381-681-3
2	2203	99.0	441	3	US-09-191-136-31
3	1554	69.8	379	3	US-09-191-136-32
4	816	36.7	388	2	US-08-742-621-1
5	813	36.5	388	3	US-09-191-608-22
6	794	35.7	388	2	US-08-750-134A-7
7	794	35.7	388	3	US-09-363-745-7
8	793	35.6	388	3	US-09-191-608-23
9	744	33.4	399	2	US-08-742-621-3
10	744	33.4	399	3	US-08-750-134A-11
11	744	33.4	399	3	US-09-363-745-11
12	739	33.2	399	2	US-08-742-621-4
13	739	33.2	399	2	US-08-750-134A-5
14	739	33.2	399	3	US-09-363-745-5
15	720	32.3	472	2	US-08-742-621-5
16	720	32.3	472	3	US-08-842-079-15
17	720	32.3	472	3	US-09-638-857-15
18	709	31.9	471	3	US-09-191-608-17
19	694	31.2	404	3	US-09-191-608-18
20	693	31.1	497	3	US-09-191-608-20
21	679.5	30.5	397	2	US-08-750-134A-9
22	679.5	30.5	397	3	US-09-363-745-9
23	679.5	30.5	397	3	US-09-191-136-17
24	673.5	30.3	397	3	US-09-191-136-16
25	631	28.3	447	3	US-09-191-608-19
26	608.5	27.3	595	3	US-08-842-079-18
27	608.5	27.3	595	3	US-08-842-079-20

Sequence 18, Appl
Sequence 20, Appl
Sequence 6, Appl
Sequence 17, Appl
Sequence 6, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 7099, Ap
Sequence 43, Appl
Sequence 69, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 11711, A

28 608.5 27.3 595 4 US-09-638-857-18
29 608.5 27.3 595 4 US-09-638-857-20
30 602.5 27.1 595 3 US-08-842-079-6
31 602.5 27.1 595 3 US-08-842-079-17
32 602.5 27.1 595 4 US-09-638-857-6
33 602.5 27.1 595 4 US-09-638-857-17
34 349 15.7 211 1 US-07-915-934-4
35 349 15.7 211 1 US-08-325-743-4
36 95.5 4.3 851 4 US-09-543-681A-7277
37 95 4.3 1041 3 US-08-898-978-2
38 95 4.3 1041 3 US-09-372-858-2
39 89.5 4.0 389 4 US-09-328-352-7099
40 87 3.9 451 4 US-09-578-063-43
41 87 3.9 470 4 US-09-578-063-69
42 86.5 3.9 352 2 US-08-483-926A-11
43 86 3.9 631 3 US-09-345-468-12
44 86 3.9 631 3 US-09-414-453A-12
45 85.5 3.8 827 4 US-09-489-039A-11711

ALIGNMENTS

RESULT 1
US-09-381-681-3
; Sequence 3, Application US/09381681
; Patent No. 6255472
; GENERAL INFORMATION:
; APPLICANT: TAKINO, Takashi
; APPLICANT: NAKAMURA, Yusuke
; TITLE OF INVENTION: HUMAN GENES
; FILE REFERENCE: Q55876
; CURRENT APPLICATION NUMBER: US/09/381.681
; CURRENT FILING DATE: 2000-01-10
; EARLIER APPLICATION NUMBER: JPA 9-093044
; EARLIER FILING DATE: 1997-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Human
; US-09-381-681-3

Query Match 99.0%; Score 2203; DB 3; Length 431;
Best Local Similarity 94.0%; Pred. No. 2.2e-235;
Matches 405; Conservative 0; Mismatches 0; Indels 26; Gaps 1;
Qy 1 MGSPGATTGGLLDYKTEK-----WALLAKGYQERDLE 34
Db 1 MGSPGATTGGLLDYKTEKVMTRNRVVGALQRLQFGIVVYVVGWALLAKGYQERDLE 60
Qy 35 PQFSIIITKLKGVSVTQIKELGNRLWDVADFVKPPQGENVFFLVTFNFTVPAQVQGRCPHEH 94
Db 61 PQFSIIITKLKGVSVTQIKELGNRLWDVADFVKPPQGENVFFLVTFNFTVPAQVQGRCPHEH 120
Qy 95 PSVPLANCWDEDCPGEGETSHGKVTQCCVFNCTHETCEIWSNCPVSGVVPSPRL 154
Db 121 PSVPLANCWDEDCPGEGETSHGKVTQCCVFNCTHETCEIWSNCPVSGVVPSPRL 180
Qy 155 AQQNFTLFKNVTFTSKFNFSKNALETWDPYFKHCRVEPOFSYCPVFRIGDLVAKA 214
Db 181 AQQNFTLFKNVTFTSKFNFSKNALETWDPYFKHCRVEPOFSYCPVFRIGDLVAKA 240
Qy 215 GTFEDALLGSGVGRVHWDCDLDGTGDSGCWPHYSFQLQKSYNFRTHHWEQGVBA 274
Db 241 GTFEDALLGSGVGRVHWDCDLDGTGDSGCWPHYSFQLQKSYNFRTHHWEQGVBA 300
Qy 275 RTLLKLYGRFDILVTGQAGKGLIPTAVLTGTGAWLGVWTFPFCOLLILLYVDREAHFYW 334
Db 301 RTLLKLYGRFDILVTGQAGKGLIPTAVLTGTGAWLGVWTFPFCOLLILLYVDREAHFYW 360
Qy 335 RTKYEEAKPKATANSVWRELALASQARLAECRLRSSAPAPTATAAGSQTPTGWPFCSS 394

Db	361	RTKYEAKAPKATANSVWRELALASQARLAECRLRSSAPAPTATAAGSQOTFGMPCPSS	420
Qy	395	DTHLPHSGSL	405
Db	421	DTHLPHSGSL	431
RESULT 2			
US-09-191-136-31			
; Sequence 31, Application US/09191136B			
; Patent No. 6214581			
; GENERAL INFORMATION:			
; APPLICANT: Abbott Laboratories			
; APPLICANT: Lynch, Kevin J.			
; APPLICANT: Burgard, Edward C.			
; APPLICANT: Van Biesen, T.			
; TITLE OF INVENTION: Nucleic Acids Encoding A Functional			
; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production			
; TITLE OF INVENTION: And Use Thereof			
; FILE REFERENCE: 6293.US.P1			
; CURRENT APPLICATION NUMBER: US/09/191,136B			
; CURRENT FILING DATE: 1998-11-13			
; EARLIER APPLICATION NUMBER: US 09/008,526			
; EARLIER FILING DATE: 1998-01-16			
; EARLIER APPLICATION NUMBER: US 09/008,185			
; EARLIER FILING DATE: 1998-01-16			
; EARLIER APPLICATION NUMBER: US 60/071,298			
; EARLIER FILING DATE: 1998-01-16			
; EARLIER APPLICATION NUMBER: US 60/071,669			
; EARLIER FILING DATE: 1998-01-16			
; NUMBER OF SEQ ID NOS: 32			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 31			
; LENGTH: 441			
; TYPE: PRT			
; ORGANISM: Homo sapiens (polypeptide)			
US-09-191-136-31			
Query Match 99.0%; Score 2203; DB 3; Length 441;			
Best Local Similarity 94.0%; Pred. No. 2,3e-235;			
Matches 405; Conservative 0; Mismatches 0; Indels 26; Gaps 1;			
Qy	1	MSPGATTGWLGDYKTEK-----WALLAKKGQERDLE	34
Db	11	MSPGATTGWLGDYKTEKYVTRNVRVYALQRLQFGIVVVVGVWALLAKKGQERDLE	70
Qy	35	POFSIITKLKGVSVTQIKELGNRLNDVADFKVPPQGENVFLVNTFLVTPAQVQGRCPH	94
Db	71	POFSIITKLKGVSVTQIKELGNRLNDVADFKVPPQGENVFLVNTFLVTPAQVQGRCPH	130
Qy	95	PSVPLANCWDEDCPEGEGGTHSHGVKTCQCVFNGTHRTCEIWSWCPVSGVPSRPLL	154
Db	131	PSVPLANCWDEDCPEGEGGTHSHGVKTCQCVFNGTHRTCEIWSWCPVSGVPSRPLL	190
Qy	155	AAQONFTLFIKNTVTFKSNFNALETWPTFYKHCVRYPQSPYCPVFRIGDLVAKA	214
Db	191	AAQONFTLFIKNTVTFKSNFNALETWPTFYKHCVRYPQSPYCPVFRIGDLVAKA	250
Qy	215	GTFEDLALLGSGVIRVHWDCLDTGDSGCWPHYSFQLOEKSYNFRATTHWSQPGVEA	274
Db	251	GTFEDLALLGSGVIRVHWDCLDTGDSGCWPHYSFQLOEKSYNFRATTHWSQPGVEA	310
Qy	275	RTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGAAMLGVVTFCDLLLLLYVDREAHFYW	334
Db	311	RTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGAAMLGVVTFCDLLLLLYVDREAHFYW	370
Qy	335	RTKYEAKAPKATANSVWRELALASQARLAECRLRSSAPAPTATAAGSQOTFGMPCPSS	394
Db	371	RTKYEAKAPKATANSVWRELALASQARLAECRLRSSAPAPTATAAGSQOTFGMPCPSS	430
Qy	395	DTHLPHSGSL	405

Db	431	DTHLPHSGSL	441
RESULT 3			
US-09-191-136-32			
; Sequence 32, Application US/09191136B			
; Patent No. 6214581			
; GENERAL INFORMATION:			
; APPLICANT: Abbott Laboratories			
; APPLICANT: Lynch, Kevin J.			
; APPLICANT: Burgard, Edward C.			
; APPLICANT: Van Biesen, T.			
; TITLE OF INVENTION: Nucleic Acids Encoding A Functional			
; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production			
; TITLE OF INVENTION: And Use Thereof			
; FILE REFERENCE: 6293.US.P1			
; CURRENT APPLICATION NUMBER: US/09/191,136B			
; CURRENT FILING DATE: 1998-11-13			
; EARLIER APPLICATION NUMBER: US 09/008,526			
; EARLIER FILING DATE: 1998-01-16			
; EARLIER APPLICATION NUMBER: US 09/008,185			
; EARLIER FILING DATE: 1998-01-16			
; EARLIER APPLICATION NUMBER: US 60/071,298			
; EARLIER FILING DATE: 1998-01-16			
; EARLIER APPLICATION NUMBER: US 60/071,669			
; EARLIER FILING DATE: 1998-01-16			
; NUMBER OF SEQ ID NOS: 32			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 32			
; LENGTH: 379			
; TYPE: PRT			
; ORGANISM: Rattus rattus			
US-09-191-136-32			
Query Match 69.8%; Score 1554; DB 3; Length 379;			
Best Local Similarity 75.7%; Pred. No. 1.8e-163;			
Matches 281; Conservative 26; Mismatches 38; Indels 26; Gaps 1;			
Qy	6	ATTGWLGDYKTEK-----WALLAKKGQERDLEPQFSI	39
Db	8	ALVSWGFLDYKTEKYVTRNCWVGISQRLQLGVVVVIGWALLAKKGQYQWMDPQISV	67
Qy	40	ITKLKGVSVTQIKELGNRLNDVADFKVPPQGENVFLVNTFLVTPAQVQGRCPHPSVPL	99
Db	68	ITKLKGVSVTQIKELGNRLNDVADFKVPPQGENVFLVNTFLVTPAQVQGRCPHPSVPL	127
Qy	100	ANCWVDEDCPEGEGGTHSHGVKTCQCVFNGTHRTCEIWSWCPVSGVVPSPLLAQON	159
Db	128	ANCWVDEDCPEGEGGTHSHGVKTCQCVFNGTHRTCEIWSWCPVSGVVPSPLLAQON	187
Qy	160	FTLFIKNTVTFKSNFNALETWPTFYKHCVRYPQSPYCPVFRIGDLVAKAGGTFE	219
Db	188	FTLFIKNTVTFKSNFNALETWPTFYKHCVRYPQSPYCPVFRIGDLVAKAGGTFE	247
Qy	220	DIALLGSGVIRVHWDCLDTGDSGCWPHYSFQLOEKSYNFRATTHWBPQGVARTLLK	279
Db	248	DIALLGSGVIRVHWDCLDTGDSGCWPHYSFQLOEKSYNFRATTHWBPQGVARTLLK	307
Qy	280	LYGIREFDILVTGQAGKFGLIPTAVTLGTGAAMLGVVTFCDLLLLLYVDREAHFYWKYE	339
Db	308	LYGIREFDILVTGQAGKFGLIPTAVTLGTGAAMLGVVTFCDLLLLLYVDREAHFYWKYE	367
Qy	340	EAKAPKATANS	350
Db	368	EAKAPKATANS	378

RESULT 4			
US-08-742-621-1			
; Sequence 1, Application US/08742621			
; Patent No. 5856129			
; GENERAL INFORMATION:			
; APPLICANT: HILLMAN, JENNIFER L.			

RESULT 5
US-09-191-608-22
; Sequence 22, Application US/09191608
; Patent No. 6242216

REPLY 6
US-08-750-134A-7
Sequence 7, Application US/08750134A
Patent No. 5985603
GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P-X RECEPTORS (PUTINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750.134A

QY 20 WALLAKGYOERDLBPQSIITKLKGVSVTOIKELGNRLWVADFKVPPQGENVFLVTN 79
Db 46 WVFWEKGYQEDT-SVSGSVITKAGVAVTNSQGFRIWDVADIVIPQAQENSLFMTN 104
QY 80 FLVTPAQVQGRCPHSPVPLANCWVDEDCPEGEGGTHSHGVKTCQCVVFNHGTHTCEIWS 139
Db 105 MIVTVNQTSTCEIPD-KTSLCNSDADCTPGSVDTSSGVATGCVFFNESVKTCEVAA 163
QY 140 WCPVESGV-VPSRPLLAQONFTLFIKNVTFTSKFNPSKNALETWDTYFKHCYBPOF 198
Db 164 WCPVENDGVPTPAFLKAAENFTLLVKNINWYKFNPSKRNLTNITTSYLKSCINYAQT 223
QY 199 SPYCPVFRIGDLVAKAGGTFFDLALLGGSGVIRVHWDCLDGTGDSGCWPHYSFQJQE--- 255
Db 224 DFPCIFRLGTIVEDAGHSFOEMAVEGGIMGQIKWDCNLOBAAASLCPLPSYFRFLDTRD 283
QY 256 -----KSNFTATHWEPQGVARTLLKLYGIRFDILVTQOAGKFGILPTAVTLGTGA 309
Db 284 LEHNVSPGNFRFAKYRDLAQEQRTLTAKYGIRFDIIVFGKAGKFDIIPMTINVGSL 343
QY 310 AMLGVVTFPCDLLLYVDREAHFYWRTKYE 339
Db 344 ALLGVATVLCVIVLYCMKKYKYDDKKYK 373

RESULT 9

US-08-742-621-3
; Sequence 3, Application US/08742621
; Patent No. 5856129
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: COLEMAN, ROGER
; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,621
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ballings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0147 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 166438
US-08-742-621-3

Query Match 33.4%; Score 744; DB 2; Length 399;

Best Local Similarity 44.0%; Pred. No. 1.5e-73;
Matches 159; Conservative 56; Mismatches 128; Indels 18; Gaps 9;
QY 20 WALLAKGYOERDLBPQSIITKLKGVSVTOIKELGNRLWVADFKVPPQGENVFLVTN 79
Db 47 WVFWEKGYQEDT-SVSGSVITKAGVAVTNSQGFRIWDVADIVIPQAQENSLFMTN 105
QY 80 FLVTPAQVQGRCPHSPVPLANCWVDEDCPEGEGGTHSHGVKTCQCVVFNHGTHTCEIWS 139
Db 106 FIVTPKOTQGYCAEHPEGGI--CKEDSGCTPGKAKRKAQGIKTKCVAFNDTVKTCIEIFG 163
QY 140 WCPVESGV-VPSRPLLAQONFTLFIKNVTFTSKFNPSKNALETWDTYFKHCYBPOF 198
Db 164 WCPVEVDDDDIPRALLREAENFTLFIKNISISFFPKVNRNRENVVEVNAAHMKTCLFHKTL 223
QY 199 SPYCPVFRIGDLVAKAGGTFFDLALLGGSGVIRVHWDCLDGTGDSGCWPHYSFQ--LQEK 256
Db 224 HPLCPVQLGVYVQESQNFSTLAEXGVVGIIDWHICDLWHVHCRPIYEFHGLYEK 283
QY 257 S-----YNFRATHWEPQGVARTLLKLYGIRFDILVTQOAGKFGILPTAVTLGTGA 312
Db 284 NLSFGNFRFAHFVEN-GTNYRHLFKVFGIRFDILVDGKAGKFDIIPMTTIGSGIGIF 342
QY 313 GVVTFFCDLLLYVDREAHFY--WRTKYEEAKAPKATANSVWRELALASQA-ELAECLRR 369
Db 343 GVATVLCDLLLHLPKRYHKOKKFKYAEKMGFGAAE-----RDLAATSTSLGQENMRT 398
RESULT 10
US-08-750-134A-11
; Sequence 11, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-750-134A-11

Query Match 33.4%; Score 744; DB 2; Length 399;

Best Local Similarity 44.0%; Pred. No. 1.5e-73;
Matches 159; Conservative 56; Mismatches 128; Indels 18; Gaps 9;

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QY 20 WALLAKKGYQERDLEPQFSIITTLKLGYSVTOIKELGNRLNVDADFVKPPQGSNNVFLVTN 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 WYFLKEGYQTSS-GLTSSVSVKLGHAUATQLPGLGQVMDVADYVYFPAQGSNVFVMTN 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 FLVTPAQQGRCPBHPSPVLANCWVDEDCPEGSGTSHGVKTGQCVWNGTHRTCEIWS 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 FIVTFKQTQGYCAEHPEGGI--CKEDSGCTPGRAKKAQGIKTKCAVFNDFVTKCIFG 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 140 WCPVE-SGVPSRPLLAQAQNFTLFIKNTVTFKFNFSKNALETWDPITYFKHCRYEQF 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 WCPVEVDDIDPALLREAENFTLFIKNSIFPRPKVNRRLVEEVAHAHMKTLCLFHKTL 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 199 SPYCPVPRIGDLVAKAGGTEDLALGGSVGIHVHWDCLDLDGDSGCPHFHSFQ--LQEK 256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 HPLCPVFGLVYVQESQNSTLAEKGGVVGITIDWHCDLDHVRHCRPIYEFHGLVEEK 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 257 S-----YNERTATHWEGPGVEARTLLKLYGIRFDILVTGQAGKFGILPTAVTLGTGAWL 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 NLSPGFNFRFARHFVEN-GTNYRHLFKVGIRFDILVDGAKGKFDIITMTTIGSGGIGF 342
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 313 GVTVPFCDLLLYVDREAHFY--WRTKYEEKAPKATANSVMRELALASQA--RLAECLLR 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 GVAIVLCDLLLHILPKRHHYKQKFKYADMGDPGAAS----FDLAATSSITGLQENWRT 398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 370 S 370
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 399 S 399
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 11
US-09-363-745-11
; Sequence 11, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-09-363-745-11

Query Match          33.4%; Score 744; DB 3; Length 399;
Best Local Similarity 44.0%; Pred. No. 1.5e-73;
Matches 159; Conservative 56; Mismatches 128; Indels 18; Gaps 9;

QY   20 WALLAKKGQERDLQPQSIIITKLKGVSTQIKELGNRLVDVADFKVPQGENVFPLVTN 79
      :|::|||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db   47 WFLFYBKGYCTSS-GUISSVSVKLGLAVTQIFGLGPQVMDVADYVFPAQGNSFVVMTN 105
      :|::|||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
QY   80 FLVTPAQVGRCRPEHPSVPLANCVDEDCPEGEGGTHSHGVTQCQWFNGTHRTCEIWS 139
      :|::|||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db   106 FIVTPQTQGYCAEHPEGGI--CKEDSGCTPGKAKEKAGIIRTKCVAINDVIKICEIFG 163
      :|::|||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
QY   140 WCPVE-SGVVSRPLLAAQNNTLFIKNVTTSKFNSKSNALETWDPITYFKHCVEPQF 198
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
Db   164 WCPVEVDDIDIPALLREAFNETLFINKSISPRFKVNRNTVEEVNAAHMKTCLFHKL 223
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
QY   199 SPYCYPFERIGDLVAKAGGTFFEDLALLGGSVGRVHWDCDLDGDSGCWPHSYFQ--LOEK 256
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
Db   224 HPLCPVFOIGYVVQSQNFSLAEKGGVVGITI DWHCDLDHHVRHCRPIYFPHGLYEK 283
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
QY   257 S----YNFTATHWEQPVGEARTLLKXIGIFDIILVTGOAKFGLIPTAVTLGTGAWL 312
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
Db   284 NLSPGFNFRFARHFVEN-GTNYRHLPKFVEGIFDIILDGKAGKDPIIPTMTTIGSIGIF 342
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
QY   313 GVUTTFCDLLLAVDREAHFY--WTKYEEAKPKATANSVRELAASQA--RLAECRLR 369
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
Db   343 GVATVLCDLLHLIPKRHYHKQKKFAEDMGPGAEE---RDIAATSTLGLQENMKT 398
      :|::|||:|:|||||:|:|||||:~::~|||:|:|||||:|:|||||:|:|||||:|:
QY   370 S 370
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Db   399 S 399
      |-----|

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RESULT 12
US-08-742-621-4
; Sequence 4, Application US/08742621
; Patent No. 5856129
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: COLEMAN, ROGER
; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,621
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0147 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 558240
US-08-742-621-4

Query Match      33.2%; Score 739; DB 2; Length 399;
Best Local Similarity 43.8%; Pred. No. 5.4e-73;
Matches 153; Conservative 60; Mismatches 114; Indels 22; Gaps 8;

QY 20 WALLAKGYQ-ERDLEPQFSITKLKGVSVTQIKELGNRLWDVADFKVPQGENVFVLVT 78
DB 47 WVFYKGYQTSSDLISVSU--KLGLAVTQGLGQVQVMDVADYVFAHGSSFFVMT 104
QY 79 NFLVTPAQVQGRCPHESVPLANCWDEDCPEGEGTHSHGKVTGQCWFVNGTHRTCEIW 138
DB 105 NFIVTPQQTQGHCAENPEGGI--CQDSSGCTPGKAERKAQGIKNCVFNPGTVKTCBIF 162
QY 139 SMCPEV-SGVVPSRPILLAAQNFITLFIKNTVTSKFNFSKNALETWDPYFKHCRYPEQ 197
DB 163 GWCPEVDDKIPSPALLAREAFNFTLFIKNSISFPRKVNRRNLVEVNGTYMKKCLYHKI 222
QY 198 FSPYCPVFRIGDLVAKAGTFFEDLALGSGVGRVHWDCDLDTGDSGCWPHYSFQ--LQE 255
DB 223 QHPLCPVFNLYGVVRESQDFRSIAEKGGVVGITIDWKCDLDMHVRHCKPIYQPHGLYGE 282
QY 256 KS-----YNFRTATHWQPGVEARTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGAAM 311
DB 283 KNLSPGFNFRFAH-FVQNGTNRHLFKVFGIHFILVDGKAGKFDIPTMTTIGSGIGI 341
QY 312 LGVVTFFCDLLLLYVDREAHFYWRTKYEAK-----APKATANSV 351
DB 342 FGVATVCLDLLLHILPKRHYKQKFKYAEDMGPGEGHDPVATSTL 390

RESULT 13
US-08-750-134A-5
; Sequence 5, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; STRANDEDNESS: linear
; MOLECULE TYPE: protein
US-08-750-134A-5

Query Match      33.2%; Score 739; DB 2; Length 399;
Best Local Similarity 43.8%; Pred. No. 5.4e-73;
Matches 153; Conservative 60; Mismatches 114; Indels 22; Gaps 8;

QY 20 WALLAKGYQ-ERDLEPQFSITKLKGVSVTQIKELGNRLWDVADFKVPQGENVFVLVT 78
DB 47 WVFYKGYQTSSDLISVSU--KLGLAVTQGLGQVQVMDVADYVFAHGSSFFVMT 104
QY 79 NFLVTPAQVQGRCPHESVPLANCWDEDCPEGEGTHSHGKVTGQCWFVNGTHRTCEIW 138
DB 105 NFIVTPQQTQGHCAENPEGGI--CQDSSGCTPGKAERKAQGIKNCVFNPGTVKTCBIF 162
QY 139 SMCPEV-SGVVPSRPILLAAQNFITLFIKNTVTSKFNFSKNALETWDPYFKHCRYPEQ 197
DB 163 GWCPEVDDKIPSPALLAREAFNFTLFIKNSISFPRKVNRRNLVEVNGTYMKKCLYHKI 222
QY 198 FSPYCPVFRIGDLVAKAGTFFEDLALGSGVGRVHWDCDLDTGDSGCWPHYSFQ--LQE 255
DB 223 QHPLCPVFNLYGVVRESQDFRSIAEKGGVVGITIDWKCDLDMHVRHCKPIYQPHGLYGE 282
QY 256 KS-----YNFRTATHWQPGVEARTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTGAAM 311
DB 283 KNLSPGFNFRFAH-FVQNGTNRHLFKVFGIHFILVDGKAGKFDIPTMTTIGSGIGI 341
QY 312 LGVVTFFCDLLLLYVDREAHFYWRTKYEAK-----APKATANSV 351
DB 342 FGVATVCLDLLLHILPKRHYKQKFKYAEDMGPGEGHDPVATSTL 390

RESULT 14
US-09-363-745-5
; Sequence 5, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; US-09-363-745-5
Query Match 33.2%; Score 739; DB 3; Length 399;
Best Local Similarity 43.8%; Pred. No. 5,4e-73;
Matches 153; Conservative 60; Mismatches 114; Indels 22; Gaps 8;
QY 20 WALLAKGVQ-BRDLEPFSIITKLKGVSVTOIKELGNRLWDVADFKVPPQGENVFLVTN 78
DB 47 WYFVYKGYTSSDISSVS--KLGLAVTQLOGLPQVMDVADYVFPAGHDSFVYMT 104
QY 79 NFLVTPAQVQGRCPHPSVPLANCWDEDCPEGEGTSHGVKTCQCVFVNGTHTCEIW 138
DB 105 NFIVTPQQTQGHCANPEGGI--CQDSDGCTPGKAERKAQGIKRTGNCVFPNGTCKEIP 162
QY 139 SWCPVE-SGVPSRPLLAQAQNTFLFKNTVTFKFNFSKNALETWDPYFKHCRYEPQ 197
DB 163 GMCPEVEDDKIPSPALLREAENFTLFIKNSISFPFRKVNRENLEVEVNGTYMKCLYHKI 222
QY 198 PSPYCPVERIGDLVAKAGTGFEDLALIGSVGIRVHWDCLDGTGSGCWPHYSFQ--LQE 255
DB 223 QHPLCPVNLGTVVRESQDFSLAEKGVVGITIDWKCDLDWVRHCKPIQFHLYGE 282
QY 256 KS-----YNFRTATHWEQPGVEARTLLKLYGIRFDILVTGQAGKFLIPTAVTLGTGA 311
DB 283 KNLSPGFNFRFARH-FVQNGTNRHLFKVFGIHFDILVDGKAGKFDIIPNTTIGSGIGI 341
QY 312 LGVTFEFDLLLYVDREAHFWRKYBEAK-----APKATANSV 351
DB 342 FGAVTLCDLLHLPRHYKQKFKYAEQMGEGEHDPVATSTL 390

RESULT 15
US-08-742-621-5
; Sequence 5, Application US/08742621
; Patent No. 5856129
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: COLEMAN, ROGER
; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,621
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0147 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 558831
; US-08-742-621-5
Query Match 32.3%; Score 720; DB 2; Length 472;
Best Local Similarity 37.4%; Pred. No. 9e-71;
Matches 144; Conservative 71; Mismatches 144; Indels 26; Gaps 5;
QY 20 WALLAKGVQERDLBPQFSIITKLKGVSVTOIKELGNRLWDVADFKVPPQGENVFLVTN 79
DB 47 YFVIVQSYQDSETGPSSIIITKVGITMSE-----DKVMDVEEYKPPGSGSVSIITR 101
QY 80 FLVTPAQVQGRCPHPSVPLANCWDEDCPEGEGTSHGVKTCQCV-FVNGTHTCEIW 138
DB 102 IEVTPSQTTLGTCPSRVRVHSSCHSDDDCIAQLDMQNGIRTGHCVPYHGDSTCEVS 161
QY 139 SWCPVESGVVPSRPLLAQAQNTFLFKNTVTFKFNFSKNALETWDPYFKHCRYEPQ 198
DB 162 AMCPVEDGTSNHLFLGKMAPNFTILIKNSIHYPKFKFSKGN-IASQKSDYLKXCTFDQDS 220
QY 199 SPYCPVFRIGDLVAKAGTGFEDLALLGSGVIRVHWDCLDGTGSGCWPHYSFQ--QE--- 255
DB 221 DYCPIFRIGFIVEKAGENFTLAHKGVGIVGIINWNCDDLDSECECKPKYSFRLLDPKY 280
QY 256 ---KSYNFRATATHWEQPGVEARTLLKLYGIRFDILVTGQAGKFLIPTAVTLGTGA 311
DB 281 DPASSGYNFRFAKYKINGTTTTTLIKAYGIRIDIVHVGQAGKFLIPTIINLATALTS 340
QY 312 LGVTFEFDLLLYVDREAHFWRKYBEAKAPKATANSVWRELALASQARLAECLERSS 371
DB 341 IGVSELCDMILLTFMKNKLYSHKKFDKVRTPKHPSGRWPVTALV-----L 388
QY 372 APAPTATAAGSOTQTPGWPCPSSDT 396
DB 389 GQIPPPSHYSQDQPPSPSGEGPT 413

Search completed: November 21, 2004, 15:05:00
Job time : 41 secs
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OM protein - protein search, using sw model

Run on: November 21, 2004, 14:41:41 ; Search time 156 Seconds
(without alignments)

931.316 Million cell updates/sec

Title: US-09-820-095b-2

Perfect score: 2226

Sequence: 1 MGSPDATTGWLLDYKTEKW.....TFGWPCPSSDTHLPHSGSL 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2226	100.0	405	6	AAO15997 Human P2X
2	2203	99.0	431	2	AAW76434 Human p53
3	2203	99.0	431	7	ADD44744 Human Pro
4	2203	99.0	441	4	AAE01141 Human P2X
5	2199	98.8	431	8	ADP49183 Human P2X
6	1554	69.8	379	4	AAE01142 Rat Purin
7	1554	69.8	379	7	ADD44742 Rat Prote
8	1552	69.7	379	2	AAW76440 Human p53
9	1444.5	64.9	310	8	ADP29439 Human sec
10	892	40.1	455	2	AAW76439 Human p53
11	825.5	37.1	422	7	ADP07989 Novel pro
12	822	36.9	422	7	ADP76897 Novel hum
13	822	36.9	422	8	ADP49181 Human P2X
14	818	36.7	404	2	AAW47067 Human bra
15	816	36.7	388	2	AAW47066 Human bra
16	816	36.7	388	2	AAW55035 HPURR ami
17	816	36.7	388	6	ADA09975 Human lig
18	816	36.7	388	8	ADH36222 Human pur
19	816	36.7	388	8	ADP49179 Human P2X
20	813	36.5	388	4	AAE84382 Amino aci
21	810	36.4	388	4	ADH1512 Human P2X
22	810	36.4	388	8	ADJ58917 Human 102
23	794	35.7	388	2	AAW04216 Rat super
24	791	35.5	388	2	AAW76438 Human p53
25	779	35.0	422	5	ABB97440 Novel hum

26	744	33.4	399	2	AAW04218 Human uri
27	744	33.4	399	7	ADA01480 Human pur
28	744	33.4	399	7	ADK52596 Hematolog
29	744	33.4	399	8	ADP49173 Human P2X
30	739	33.2	399	2	AAW04215 Rat vas d
31	739	33.2	399	2	AAW76435 Human p53
32	726	32.6	440	8	ADH22560 Human tra
33	720	32.3	472	2	AAW76436 Human p53
34	720	32.3	472	4	AAE28252 P2X 2. 2/
35	720	32.3	472	7	ADA09824 Rat_P2X2
36	720	32.3	472	8	ADP49175 Rat P2X2
37	709	31.9	459	7	AAE38586 Human ion
38	709	31.9	471	3	AAE70274 Human pur
39	709	31.9	471	4	AAE84378 Amino aci
40	706.5	31.7	373	8	ADP29741 Human sec
41	704.5	31.6	397	6	ABR59707 Human ion
42	704.5	31.6	397	7	ADJ70396 Human hea
43	694	31.2	402	4	AAU87387 Novel cen
44	694	31.2	402	8	ADI54702 Novel hum
45	694	31.2	404	3	AAE70275 Human pur

ALIGNMENTS

RESULT 1

AAO15997
ID AAO15997 standard; protein; 405 AA.

XX AC AAO15997;

DT 20-FEB-2003 (first entry)

XX DE Human P2X-like purinergic receptor G-protein coupled receptor.

XX KW Human; gene therapy; G-protein coupled receptor; chromosome 22;

XX KW P2X-like purinergic receptor; anaplastic oligodendrogloma; GPCR;

XX KW chronic lymphocytic leukaemia; lung carcinoma; colon carcinoma;

XX KW brain carcinoma; drug screening; tissue typing; pharmacogenomic analysis;

XX KW single nucleotide polymorphism; SNP.

XX OS Homo sapiens.

XX PN WO200279229-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002MO-US009545.

XX PR 29-MAR-2001; 2001US-00820095.

XX PA (PEKE) PE CORP NY.

XX FI Wei M, Gong F, Di Francesco V, Beasley EM;

XX DR WPI; 2003-040648/03.

XX DR N-PSDB; AAL51048, AAL51049.

XX PT New peptides related to P2X-like purinergic receptor subfamily, useful for

XX PT treating disorders associated with abnormal expression of protease in

XX PT anaplastic oligodendrogloma, leukemia, carcinoma lung, or large cell

XX PS lung carcinoma.

XX PS Claim 1; Fig 2A; 87pp; English.

XX CC The invention comprises the amino acid and coding sequence (located on

XX CC chromosome 22) of a human G-protein coupled receptor (GPCR) which is

XX CC related to the P2X-like purinergic receptor subfamily. The DNA and

XX CC protein sequences of the invention are useful for treating: anaplastic

XX CC oligodendrogloma; chronic lymphocytic leukaemia; lung carcinoma; colon

XX CC carcinoma; and brain carcinoma. The DNA and protein sequences of the

XX CC invention are also useful for drug screening assays, tissue typing and

XX CC pharmacogenomic analysis. The present amino acid sequence represents the

CC human GPCR that is related to the P2X-like purinergic receptor subfamily
 XX
 SQ Sequence 405 AA;
 Query Match 100.0%; Score 2226; DB 6; Length 405;
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSPGATTGWLGDYKTEKALLAKGQBERDLEPQSIITKLKGVSVTQIKELGNRLWD 60
 DB 1 MGSPGATTGWLGDYKTEKALLAKGQBERDLEPQSIITKLKGVSVTQIKELGNRLWD 60
 QY 61 VADFVKPPQGENVFFLVNTFLVTPAQVQRCPEHPSVPLANCWVDEDCPEGEGTHSHGV 120
 DB 61 VADFVKPPQGENVFFLVNTFLVTPAQVQRCPEHPSVPLANCWVDEDCPEGEGTHSHGV 120
 QY 121 KTGQCVVNGTHRTCEIWSWCPVSGVVPSPPLAQAQNTLFIKNTVTSKFNFSKNA 180
 DB 121 KTGQCVVNGTHRTCEIWSWCPVSGVVPSPPLAQAQNTLFIKNTVTSKFNFSKNA 180
 QY 181 LETWDPYFKHCRVPEQSPYCPVFRIGDLVAKAGGFEDLALGGSGVIRVHWDCLDT 240
 DB 181 LETWDPYFKHCRVPEQSPYCPVFRIGDLVAKAGGFEDLALGGSGVIRVHWDCLDT 240
 QY 241 GDSGCWPHYSFQLOEKSYNFRATTHWEPQGVBEARTLLKLYGIRFDILVTGQAGKGLIP 300
 DB 241 GDSGCWPHYSFQLOEKSYNFRATTHWEPQGVBEARTLLKLYGIRFDILVTGQAGKGLIP 300
 QY 301 TAVTLGTGAALGVVTPFCDDLLLVVDREAHFYWRTKYEEAKAPKATANSVWRELALASQ 360
 DB 301 TAVTLGTGAALGVVTPFCDDLLLVVDREAHFYWRTKYEEAKAPKATANSVWRELALASQ 360
 QY 361 ARLAECLRRSSAPATAAGSQTQTPGWPSPSSDTHLPTHSGSL 405
 DB 361 ARLAECLRRSSAPATAAGSQTQTPGWPSPSSDTHLPTHSGSL 405
 RESULT 2
 AAW76434
 ID AAW76434 standard; protein; 431 AA.
 XX
 AC AAW76434;
 XX
 DT 28-APR-1999 (first entry)
 XX
 DE Human p53 regulated protein, P2XM.
 XX
 KW Human; p53 regulated protein; P2XM; ATP receptor; RP-2 protein;
 KW thymocyte; apoptosis; tumour-suppressor gene; rhabdoid sarcoma;
 KW anticancer drug.
 XX
 OS Homo sapiens.
 XX
 PN WO9842835-A1.
 XX
 PD 01-OCT-1998.
 XX
 PF 18-MAR-1998; 98WO-JP001146.
 XX
 PR 26-MAR-1997; 97JP-00093044.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 PI Tokino T, Nakamura Y;
 XX
 DR WPI; 1998-532006/45.
 DR N-P5DB; AAV61832, AAV61833.
 XX
 PT Human gene P2XM whose transcription is induced by p53 - useful, e.g. for
 PT diagnostic purposes and in development of new anticancer drugs.
 XX
 PS Claim 1; Page 23-27; 43pp; Japanese.

CC This sequence represents the P2XM protein of the invention. The protein
 CC is significantly homologous to: (i) the P2X family of ATP receptors, and
 CC (ii) RP-2 protein which is expressed in thymocytes during apoptosis.
 CC Transcription of the genes is specifically regulated by the tumour-
 CC suppressor gene p53. The P2XM gene is specifically expressed in skeletal
 CC muscle and has been localised to chromosome 22q11, an area where mutation
 CC and sequence losses frequently occur in rhabdoid sarcomas. The genes may
 CC be used for diagnostic purposes (e.g. by detecting changes occurring in
 CC the gene in sarcomas), using probes and primers containing or derived
 CC from all or part of the genes. The genes may further be used in the
 CC development of new anticancer drugs
 XX
 SQ Sequence 431 AA;
 Query Match 99.0%; Score 2203; DB 2; Length 431;
 Best Local Similarity 94.0%; Pred. No. 7.8e-208;
 Matches 405; Conservative 0; Mismatches 0; Indels 26; Gaps 1;
 QY 1 MGSPGATTGWLGDYKTEK-----WALLAKKGYOERDLE 34
 DB 1 MGSPGATTGWLGDYKTEKYVNRVNRVGLQRLQFGIVVVGWALLAKKGYOERDLE 60
 QY 35 POFSIITKLKGVSVTQIKELGNRLWDVADFVKPPQGENVFFLVNTFLVTPAQVQRCPEH 94
 DB 61 POFSIITKLKGVSVTQIKELGNRLWDVADFVKPPQGENVFFLVNTFLVTPAQVQRCPEH 120
 QY 95 PSVPLANCWVDEDCPEGEGTHSHGVKTGCQVFNHGTHTCEIWSWCPVSGVVPSPRL 154
 DB 121 PSVPLANCWVDEDCPEGEGTHSHGVKTGCQVFNHGTHTCEIWSWCPVSGVVPSPRL 180
 QY 155 AQAQNTLFIKNTVTSKFNFSKNALETWDPYFKHCRVPEQSPYCPVFRIGDLVAKA 214
 DB 181 AQAQNTLFIKNTVTSKFNFSKNALETWDPYFKHCRVPEQSPYCPVFRIGDLVAKA 240
 QY 215 GGTFFEDLALGGSGVIRVHWDCLDTGSGCWPHYSFQLOEKSYNFRATTHWEPQGV 274
 DB 241 GGTFFEDLALGGSGVIRVHWDCLDTGSGCWPHYSFQLOEKSYNFRATTHWEPQGV 300
 QY 275 RTLLKLYGIRFDILVTGQAGKGLIPTAVTLGTGAALGVVTPFCDDLLLVVDREAHFYW 334
 DB 301 RTLLKLYGIRFDILVTGQAGKGLIPTAVTLGTGAALGVVTPFCDDLLLVVDREAHFYW 360
 QY 335 RTKYEEAKAPKATANSVWRELALASQARLAECLRRSSAPATAAGSQTQTPGWPSPSS 394
 DB 361 RTKYEEAKAPKATANSVWRELALASQARLAECLRRSSAPATAAGSQTQTPGWPSPSS 420
 QY 395 DTHLPTHSGSL 405
 DB 421 DTHLPTHSGSL 431
 RESULT 3
 ADD44744
 ID ADD44744 standard; protein; 431 AA.
 XX
 AC ADD44744;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein NP_005437, SEQ ID NO 10173.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; NP_005437.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 431 AA;
 Query Match 99.0%; Score 2203; DB 7; Length 431;
 Best Local Similarity 94.0%; Pred. No. 7.8e-208;
 Matches 405; Conservative 0; Mismatches 0; Indels 26; Gaps 1;
 QY 1 MGSPGATTCGGLLDYKTEK-----WALLAKGYQERDLE 34
 DB 1 MGSPGATTCGGLLDYKTEKYNVTRNRVGLQRLQFGIVVVGWALLAKGYQERDLE 60
 QY 35 POFSIITKLKGVSVTQIKELGNRLNDVADVPQGENVFFLVTLVTPAQVQRCPEH 94
 DB 61 POFSIITKLKGVSVTQIKELGNRLNDVADVPQGENVFFLVTLVTPAQVQRCPEH 120
 QY 95 PSVPLANCWVDDCEGEGCTHSHGVKTCQCVVFNGTHTCTIMSWCPVSGVWPSRPLL 154
 DB 121 PSVPLANCWVDDCEGEGCTHSHGVKTCQCVVFNGTHTCTIMSWCPVSGVWPSRPLL 180
 QY 155 AQAQNTFLIKNTVTFKFNFSKNALETWDTYFKHCRIYEPQFPYCPFRIGDLVAKA 214
 DB 181 AQAQNTFLIKNTVTFKFNFSKNALETWDTYFKHCRIYEPQFPYCPFRIGDLVAKA 240
 QY 215 GGTFFEDALLGGSVGRVHWDCLDTGDSGCWPHYSFQLOEKSYNFRATHTHWEOPGVEA 274
 DB 241 GGTFFEDALLGGSVGRVHWDCLDTGDSGCWPHYSFQLOEKSYNFRATHTHWEOPGVEA 300
 QY 275 RTLLKLYGIRFDILVTGQAGKGLIPTAVTLGTGAANLGVVTFPCDLLLLLYVDREAHFYW 334

Db 301 RTLLKLYGIRFDILVTGQAGKGLIPTAVTLGTGAANLGVVTFPCDLLLLLYVDREAHFYW 360
 QY 335 RTKYEEAKAPKATANSVWRELALASQARLAECRLRRSSAPAPTATAAGSQTPTGWPDPSS 394
 Db 361 RTKYEEAKAPKATANSVWRELALASQARLAECRLRRSSAPAPTATAAGSQTPTGWPDPSS 420
 QY 395 DTHLPTHSGSL 405
 Db 421 DTHLPTHSGSL 431
 RESULT 4
 AAE01141
 ID AAE01141 standard; protein; 441 AA.
 XX
 AC AAE01141;
 DT 17-JUL-2001 (first entry)
 DE Human purinergic receptor P2X6 protein.
 XX
 KW Human; purinergic receptor; P2X6; antidepressant; vulnerary; hypotensive;
 KW anticonvulsant; antiinflammatory; therapy; nervous system disorder;
 KW epilepsy; pain; depression; neurodegenerative disorder; cystic fibrosis;
 KW neuromuscular disease; reproductive system disorder; hypertension;
 KW peripheral vascular disease; immune system disorder; chronic bronchitis;
 KW irritable bowel disorder; premature ejaculation; asthma.
 XX
 OS Homo sapiens.
 XX
 PN USC214581-B1.
 XX
 PD 10-APR-2001.
 XX
 PF 13-NOV-1998; 98US-00191136.
 XX
 PR 16-JAN-1998; 98US-00008185.
 PR 16-JAN-1998; 98US-00008526.
 PR 16-JAN-1998; 98US-0071298P.
 PR 16-JAN-1998; 98US-0071669P.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Lynch KJ, Burgard EC, Van Biesen T;
 XX
 DR WPI; 2001-315459/33.
 DE N-PSDB; RAD04978.
 XX
 PT Novel isolated polynucleotide encoding human purinergic P2X3 receptor
 PT polypeptide useful for identifying potentially therapeutic compounds that
 PT modulate or otherwise interact with P2X containing receptors.
 XX
 PS Example 9; Fig 9; 53pp; English.
 XX
 CC The present sequence is human P2X6 purinergic receptor protein. P2X
 CC receptors are ligand-gated ion channels while P2Y receptors operate
 CC generally through a G-protein coupled system. P2X purinoreceptor drugs
 CC are potential therapeutic agents in several disorders including central
 CC nervous system or peripheral nervous system conditions, e.g., epilepsy,
 CC pain, depression, neurodegenerative disorders, disorders of the skeletal
 CC muscle such as neuromuscular diseases, disorders of the reproductive
 CC system, asthma, peripheral vascular disease, hypertension, immune system
 CC disorders, irritable bowel disorder, premature ejaculation, cystic
 CC fibrosis and chronic bronchitis. P2Y purinoreceptors mediate the activity
 CC of extracellular nucleotide triphosphates to regulate chloride secretion
 CC in human airway epithelia
 XX
 SQ Sequence 441 AA;
 Query Match 99.0%; Score 2203; DB 4; Length 441;
 Best Local Similarity 94.0%; Pred. No. 8.1e-208;
 Matches 405; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MGSPGATTGGLLDYKTEK-----WALLAKGYQERDLE 34
 Db 11 MGSPGATTGGLLDYKTEKYVTRNRVGAQRLLQFGIVVVGWALLAKGYQERDLE 70
 QY 35 POFSIITKLKGVSVTQIKELGNRLMDVADFVKPQGENVFFLVTNFLTTPAQVQGRCPHEH 94
 Db 71 POFSIITKLKGVSVTQIKELGNRLMDVADFVKPQGENVFFLVTNFLTTPAQVQGRCPHEH 130
 QY 95 PSVPLANCWVDEDCPEGEGGTHSHGVKTGCQVFNHGTCTCEIWSWCPVSGVPSRPLL 154
 Db 131 PSVPLANCWVDEDCPEGEGGTHSHGVKTGCQVFNHGTCTCEIWSWCPVSGVPSRPLL 190
 QY 155 AQAQNFITLFIKNTVTFKSNFNSKNALETWDPFTYFKHCRYPQSPYCPVFRIGDLVAKA 214
 Db 191 AQAQNFITLFIKNTVTFKSNFNSKNALETWDPFTYFKHCRYPQSPYCPVFRIGDLVAKA 250
 QY 215 GGTFFEDLALLGGSGVIRVHWDCLDTGDSGCWPHYSFQLEKSYNFRATATHWQPGVEA 274
 Db 251 GGTFFEDLALLGGSGVIRVHWDCLDTGDSGCWPHYSFQLEKSYNFRATATHWQPGVEA 310
 QY 275 RTLLKLYGIRFDILVTGQAGKFGELIPTAVTLGTGAWLGVVTFDCDLLLLLYVDREAHFYW 334
 Db 311 RTLLKLYGIRFDILVTGQAGKFGELIPTAVTLGTGAWLGVVTFDCDLLLLLYVDREAHFYW 370
 QY 335 RTKYEEAKAPKATANSVWRELALASQARLAELCLRRSSAPAPTATAAGSQTOTPGWPCPSS 394
 Db 371 RTKYEEAKAPKATANSVWRELALASQARLAELCLRRSSAPAPTATAAGSQTOTPGWPCPSS 430
 QY 395 DTHLPTHSGSL 405
 Db 431 DTHLPTHSGSL 441

RESULT 5

ADP49183
 ID ADP49183 standard; protein; 431 AA.
 XX AC ADP49183;
 XX DT 26-AUG-2004 (first entry)
 XX DE Human P2X6 purinergic receptor protein sequence for odour modulation.
 XX KW odour sensitivity; P2X purinergic receptor; P2Y purinergic receptor;
 XX KW signal transduction pathway; olfactory signalling; micro-array.
 XX OS Homo sapiens.
 XX PN WO2004047749-A2.
 XX PD 10-JUN-2004.
 XX PF 21-NOV-2003; 2003WO-US037389.
 XX PR 21-NOV-2002; 2002US-0428140P.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Lucero M, Hegg C;
 XX DR WPI; 2004-460642/43.
 XX PT Modulating odor sensitivity in a subject, comprises administering a
 PT composition comprising an agonist or antagonist of P2X or P2Y purinergic
 PT receptor to the subject.
 XX PS Disclosure; SEQ ID NO 12; 108pp; English.
 XX CC The invention relates to a method of modulating (M1) odour sensitivity in
 CC a subject, by administering a composition which is an agonist or
 CC antagonist of a P2X or P2Y purinergic receptor. (M1) is useful for
 CC modulating odour sensitivity in a subject (claimed). The compositions
 CC used for modulating odour sensitivity in a subject are useful for

CC studying the signal transduction pathways related to olfactory signaling.
 CC The compositions are also useful as reagents in micro-arrays or as
 CC reagents to probe or analyze existing micro-arrays. This sequence
 CC corresponds to the human P2X6 protein sequence.

XX Sequence 431 AA;

Query Match 98.8%; Score 2199; DB 8; Length 431;
 Best Local Similarity 93.7%; Pred. No. 1.9e-207;
 Matches 404; Conservative 0; Mismatches 1; Indels 26; Gaps 1;

QY 1 MGSPGATTGGLLDYKTEK-----WALLAKGYQERDLE 34
 Db 1 MGSPGATTGGLLDYKTEKYVTRNRVGAQRLLQFGIVVVGWALLAKGYQERDLE 60
 QY 35 POFSIITKLKGVSVTQIKELGNRLMDVADFVKPQGENVFFLVTNFLTTPAQVQGRCPHEH 94
 Db 61 POFSIITKLKGVSVTQIKELGNRLMDVADFVKPQGENVFFLVTNFLTTPAQVQGRCPHEH 120
 QY 95 PSVPLANCWVDEDCPEGEGGTHSHGVKTGCQVFNHGTCTCEIWSWCPVSGVPSRPLL 154
 Db 121 PSVPLANCWVDEDCPEGEGGTHSHGVKTGCQVFNHGTCTCEIWSWCPVSGVPSRPLL 180
 QY 155 AQAQNFITLFIKNTVTFKSNFNSKNALETWDPFTYFKHCRYPQSPYCPVFRIGDLVAKA 214
 Db 181 AQAQNFITLFIKNTVTFKSNFNSKNALETWDPFTYFKHCRYPQSPYCPVFRIGDLVAKA 240
 QY 215 GGTFFEDLALLGGSGVIRVHWDCLDTGDSGCWPHYSFQLEKSYNFRATATHWQPGVEA 274
 Db 241 GGTFFEDLALLGGSGVIRVHWDCLDTGDSGCWPHYSFQLEKSYNFRATATHWQPGVEA 300
 QY 275 RTLLKLYGIRFDILVTGQAGKFGELIPTAVTLGTGAWLGVVTFDCDLLLLLYVDREAHFYW 334
 Db 301 RTLLKLYGIRFDILVTGQAGKFGELIPTAVTLGTGAWLGVVTFDCDLLLLLYVDREAHFYW 360
 QY 335 RTKYEEAKAPKATANSVWRELALASQARLAELCLRRSSAPAPTATAAGSQTOTPGWPCPSS 394
 Db 361 RTKYEEAKAPKATANSVWRELALASQARLAELCLRRSSAPAPTATAAGSQTOTPGWPCPSS 420
 QY 395 DTHLPTHSGSL 405
 Db 421 DTHLPTHSGSL 431

RESULT 6

AAE01142
 ID AAE01142 standard; protein; 379 AA.
 XX AC AAE01142;
 XX DT 17-JUL-2001 (first entry)

XX Rat purinergic receptor P2X6 protein.

Rat; purinergic receptor; P2X6; antidepressant; vulnerary; hypotensive;
 anticonvulsant; antiinflammatory; therapy; nervous system disorder;
 epilepsy; pain; depression; neurodegenerative disorder; cystic fibrosis;
 neuromuscular disease; reproductive system disorder; hypertension;
 peripheral vascular disease; immune system disorder; chronic bronchitis;
 irritable bowel disorder; premature ejaculation; asthma.

XX Rattus sp.

XX US6214581-B1.

XX 10-APR-2001.

XX 13-NOV-1998; 98US-00191136.

XX 16-JAN-1998; 98US-00008185.

XX 16-JAN-1998; 98US-00008526.

XX 16-JAN-1998; 98US-0071298P.

XX 16-JAN-1998; 98US-0071669P.

XX PA (ABBO) ABBOTT LAB.
 XX PI Lynch KJ, Burgard EC, Van Biesen T;
 XX DR WPI; 2001-315459/33.
 XX PT Novel isolated polynucleotide encoding human purinergic P2X3 receptor
 XX PT polypeptide useful for identifying potentially therapeutic compounds that
 XX PT modulate or otherwise interact with P2X containing receptors.
 XX PS Example 9; Fig 9; 53pp; English.
 XX CC The present sequence is rat P2X6 purinergic receptor protein. P2X
 CC receptors are ligand-gated ion channels while P2X purinergic receptors
 CC generally through a G-protein coupled system. P2X purinergic receptors
 CC are potential therapeutic agents in several disorders including central
 CC nervous system or peripheral nervous system conditions, e.g., epilepsy,
 CC pain, depression, neurodegenerative disorders, disorders of the skeletal
 CC muscle such as neuromuscular diseases, disorders of the reproductive
 CC system, asthma, peripheral vascular disease, hypertension, immune system
 CC disorders, irritable bowel disorder, premature ejaculation, cystic
 CC fibrosis and chronic bronchitis. P2X purinergic receptors mediate the activity
 CC of extracellular nucleotide triphosphates to regulate chloride secretion
 CC in human airway epithelia
 XX SQ Sequence 379 AA;

Query Match 69.8%; Score 1554; DB 4; Length 379;
 Best Local Similarity 75.7%; Pred. No. 5.8e-144;
 Matches 281; Conservative 26; Mismatches 38; Indels 26; Gaps 1;

QY 6 ATTGGLLDYKTEK-----WALLAKKGQERDLBPQFSI 39
 DB 8 ALVSWGFLDYKTEKYMTNRNCWGISQRLQLQGVVYVIGWALLAKKGQERDMDPQISV 67
 QY 40 ITKLKGVSVTQIKELGNRLNDVADFVKPPQGENVFLVNTVTPAQVQGRCPHEPSVPL 99
 DB 68 ITKLKGVSVTQVKELEKRLNDVADFVRPQGENVFLVNTVTPAQVQGRCPHEPSVPL 127
 QY 100 ANCWDEDCEPEGEGGTHSHGVKTCQCVFNGTHTCTEINSWCPVSGVSPRLLAQON 159
 DB 128 ANCWADEDCEPEGEGGYSHGKTCQCVAFNGTHTCTEINSWCPVSGVSPRLLAQON 187
 QY 160 FTLFKNTVTFKFNFSKNALETWDPVTFKHCRYPEQSPYCPVFRIGDLVAKAGTPE 219
 DB 188 FTLFKNTVTFKFNFSRNTALDWDNTYFKYCLVDSUSSPCVFRIGDLVAMTGGDFE 247
 QY 220 DLALLGSGVIRVHWDCLDLDGSGCWPHYSFQLQEKSYNPRATATHWEQPGVEARTLLK 279
 DB 248 DLALLGGAVGINHWDCLDLDGSGCWPHYSFQLQERGINPRATANYWAAAGVSGRSJLK 307
 QY 280 LYGIRFDILVTGQAGKFLIPTAVTLGTGAAMLGWTFPCDLLLLYVDREAHFYRTKYE 339
 DB 308 LYGIRFDILVTGQAGKFLIPTAVTGTGAAMLGWTFPCDLLLLYVDREAGFYRTKYE 367
 QY 340 EAKAPKATANS 350
 DB 368 EAKAPKATNS 378

RESULT 7
 ADD44742
 ID ADD44742 standard; protein; 379 AA.
 XX AC ADD44742;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat Protein P51579, SEQ ID NO 10171.
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PA (FARB) BAYER AG.
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P51579.
 XX New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 379 AA;

Query Match 69.8%; Score 1554; DB 7; Length 379;
 Best Local Similarity 75.7%; Pred. No. 5.8e-144;
 Matches 281; Conservative 26; Mismatches 38; Indels 26; Gaps 1;

QY 6 ATTGGLLDYKTEK-----WALLAKKGQERDLBPQFSI 39
 DB 8 ALVSWGFLDYKTEKYMTNRNCWGISQRLQLQGVVYVIGWALLAKKGQERDMDPQISV 67
 QY 40 ITKLKGVSVTQIKELGNRLNDVADFVKPPQGENVFLVNTVTPAQVQGRCPHEPSVPL 99
 DB 68 ITKLKGVSVTQVKELEKRLNDVADFVRPQGENVFLVNTVTPAQVQGRCPHEPSVPL 127
 QY 100 ANCWDEDCEPEGEGGTHSHGVKTCQCVFNGTHTCTEINSWCPVSGVSPRLLAQON 159
 DB 128 ANCWADEDCEPEGEGGYSHGKTCQCVAFNGTHTCTEINSWCPVSGVSPRLLAQON 187
 QY 160 FTLFKNTVTFKFNFSKNALETWDPVTFKHCRYPEQSPYCPVFRIGDLVAKAGTPE 219

Db 188 FTLFKNTVTNFKNFRTNALDWTNDNTYFKYCLYDLSLSSPYCVFVRIGDLVAMTGGDFE 247
 QY 220 DLALLGGSGVIRVHWDCLDITGDSGCMWPHYSFQIQEKSYNFRTATHWQEPGVEARTLLK 279
 Db 248 DLALLGGVGINIHWCNLDITKSDCSPOYSFQIQEGRYFRTANYWAAAGVBSRLK 307
 QY 280 LYGIRFDILVTGQAGKFGLIPTAVTLGTGAALWGVVTFPCDLLLLLYVDREAHFYWRKYE 339
 Db 308 LYGIRFDILVTGQAGKFPALPTAITVGTGAALWGVVTFPCDLLLLLYVDREAGFYWRKYE 367
 QY 340 EAKAPKATANS 350
 Db 368 EAPAPKATNS 378
 RESULT 8
 AAW76440
 ID AAW76440 standard; protein; 379 AA.
 XX
 AC AAW76440;
 XX
 DT 28-APR-1999 (first entry)
 XX
 DE Human p53 regulated protein, P2X6.
 XX
 KW Human; p53 regulated protein; P2XM; ATP receptor; RP-2 protein;
 KW thymocyte; apoptosis; tumour-suppressor gene; thaboid sarcoma;
 KW anticancer drug.
 XX
 OS Homo sapiens.
 XX
 PN WO9842835-A1.
 XX
 PD 01-OCT-1998.
 XX
 PF 18-MAR-1998; 98WO-JP001146.
 XX
 PR 26-MAR-1997; 97JP-00093044.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 PI Tokino T, Nakamura Y;
 XX
 DR WPI; 1998-532006/45.
 XX
 PT Human gene P2XM whose transcription is induced by p53 - useful, e.g. for
 PT diagnostic purposes and in development of new anticancer drugs.
 XX
 PS Disclosure; Fig 5-6; 43pp; Japanese.
 XX
 CC This sequence represents the human P2X6 protein. The invention relates to
 CC the P2XM protein, which is significantly homologous to: (i) the P2X
 CC family of ATP receptors, and (ii) RP-2 protein which is expressed in
 CC thymocytes during apoptosis. Transcription of the genes is specifically
 CC regulated by the tumour-suppressor gene p53. The P2XM gene is
 CC specifically expressed in skeletal muscle and has been localised to
 CC chromosome 22q11, an area where mutation and sequence losses frequently
 CC occur in thaboid sarcomas. The genes may be used for diagnostic purposes
 CC (e.g. by detecting changes occurring in the gene in sarcomas), using
 CC probes and primers containing or derived from all or part of the genes.
 CC The genes may further be used in the development of new anticancer drugs
 XX
 SQ Sequence 379 AA;
 Query Match 69.7%; Score 1552; DB 2; Length 379;
 Best Local Similarity 75.7%; Pred. No. 9.1e-144;
 Matches 281; Conservative 26; Mismatches 38; Indels 26; Gaps 1;
 QY 6 ATTGWLDDYKTEK-----WALLAKGYQERDLEPQPSI 39
 Db 8 ALVSWGFLDYKTEKYMTNFWNCVIGISORLLQLGVVVVIGWALLAKGYQEWMDPQISV 67

QY 40 ITKLKGVSVTQIKELGNRLWDVADFVKPQGENVFFLVNTFLVTPAQVQGRCPHPSPVPL 99
 Db 68 ITKLKGVSVTQIKELKRLWDVADFVRPSQGENVFFLVNTFLVTPAQVQGRCPHPSPVPL 127
 QY 100 ANCWVDEDCPEGEGGTHSHGVKTCQVVFNGFHTCEIWSWCPVSSGVVSRPRLAQON 159
 Db 128 ANCWVDEDCPEGEMGTSHGIKTGCVAFNGFHTCEIWSWCPVSSGVVSRPRLAQON 187
 QY 160 FTLFKNTVTNFKNFRTNALDWTNDNTYFKYCLYDLSLSSPYCVFVRIGDLVAMTGGDFE 219
 Db 188 FTLFKNTVTNFKNFRTNALDWTNDNTYFKYCLYDLSLSSPYCVFVRIGDLVAMTGGDFE 247
 QY 220 DLALLGGSGVIRVHWDCLDITGDSGCMWPHYSFQIQEKSYNFRTATHWQEPGVEARTLLK 279
 Db 248 DLALLGGVGINIHWCNLDITKSDCSPOYSFQIQEGRYFRTANYWAAAGVBSRLK 307
 QY 280 LYGIRFDILVTGQAGKFGLIPTAVTLGTGAALWGVVTFPCDLLLLLYVDREAHFYWRKYE 339
 Db 308 LYGIRFDILVTGQAGKFPALPTAITVGTGAALWGVVTFPCDLLLLLYVDREAGFYWRKYE 367
 QY 340 EAKAPKATANS 350
 Db 368 EAPAPKATNS 378
 RESULT 9
 ADP29439
 ID ADP29439 standard; protein; 310 AA.
 XX
 AC ADP29439;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human secreted protein SEQ ID #206.
 XX
 KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
 KW cancer; inflammatory; immune; human secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035732-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 28-AUG-2003; 2003WO-US026780.
 XX
 PR 29-AUG-2002; 2002US-0406576P.
 PR 29-AUG-2002; 2002US-0406579P.
 PR 29-AUG-2002; 2002US-0406585P.
 PR 29-AUG-2002; 2002US-0406588P.
 PR 29-AUG-2002; 2002US-0406608P.
 PR 29-AUG-2002; 2002US-0406611P.
 PR 29-AUG-2002; 2002US-0406612P.
 PR 29-AUG-2002; 2002US-0406616P.
 PR 29-AUG-2002; 2002US-0406640P.
 PR 29-AUG-2002; 2002US-0406642P.
 PR 29-AUG-2002; 2002US-0406646P.
 PR 29-AUG-2002; 2002US-0406653P.
 PR 29-AUG-2002; 2002US-0406655P.
 PR 29-AUG-2002; 2002US-0406666P.
 PR 17-SEP-2002; 2002US-0410947P.
 PR 17-SEP-2002; 2002US-0410949P.
 PR 17-SEP-2002; 2002US-0410949P.
 PR 17-SEP-2002; 2002US-0410953P.
 PR 17-SEP-2002; 2002US-0410957P.
 PR 17-SEP-2002; 2002US-0410958P.
 PR 17-SEP-2002; 2002US-0410959P.
 PR 17-SEP-2002; 2002US-0410960P.
 PR 17-SEP-2002; 2002US-0410961P.
 PR 17-SEP-2002; 2002US-0410962P.
 PR 17-SEP-2002; 2002US-0411019P.
 PR 17-SEP-2002; 2002US-0411022P.

D	b	1	WGLLDYKTEKYVWTRNRVGVGALQELLFGIIVVVVGVWALLAKKGVOERDLEPQFSIITKL	60
Q	y	44	KGVSVTQIKELGNRLWDVADFKVPQGENVFFLVTNFLVTPAOVQGRCPVHPSVPLANCW	103
D	b	61	KGVSVTQIKELGNRLWDVADFKVPQGENVFFLVTNFLVTPAOVQGRCPVHPSVPLANCW	120
Q	y	104	VBDPCPEGGGTHSHGVTKGCVVFNQTHRTCEIWSWCPVSGVPSRPLLAQAQNFTLLF	163
D	b	121	VBDPCPEGGGTHSHGVTKGCVVFNQTHRTCEIWSWCPVSGVPSRPLLAQAQNFTLLF	179
Q	y	164	IKNTVTFSEKFNFSKNALETWDPYFKHCRYPQFSYPCVFRIGDILVAKAGTFFEDLAL	223
D	b	180	IKNTVTFSEKFNFSKNALETWDPYFKHCRYPQFSYPCVFRIGDILVAKAGTFFEDLAL	209
Q	y	224	LGSGVGIRVHMDCLDTGSCWCPHYFQLEKSYNFRATATHWWEQPGVEARTLLKLYGI	283
D	b	210	LGSGVGIRVHMDCLDTGSCWCPHYFQLEKSYNFRATATHWWEQPGVEARTLLKLYGI	269
Q	y	284	RDILVTGQAGKFGLIPTAVTLGTGAWLGV	314
D	b	270	RDILVTGQAGKFGLIPTAVTLGTGAWLGV	300
RESULT 10				
AAW76439				
ID	AAW76439 standard; protein; 455 AA.			
XX	AAW76439;			
AC	AAW76439;			
XX	XX			
DT	28-APR-1999 (first entry)			
XX	XX			
DE	Human p53 regulated protein, P2X5.			
XX	XX			
KW	Human, p53 regulated protein; P2X5; ATP receptor; RP-2 protein;			
KW	thymocyte; apoptosis; tumour-suppressor gene; rhabdoid sarcoma;			
KW	anticancer drug.			
XX	XX			
OS	Homo sapiens.			
XX	XX			
PN	WO9842835-A1.			
XX	XX			
PD	01-OCT-1998.			
XX	XX			
XX	18-MAR-1998; 98WO-JP001146.			
XX	XX			
PR	26-MAR-1997; 97JP-00093044.			
XX	XX			
PA	(SAKA) OTSUKA PHARM CO LTD.			
XX	XX			
PI	Tokino T, Nakamura Y;			
PI	WPI; 1998-532006/45.			
DR	XX			
PT	Human gene P2X5 whose transcription is induced by p53 - useful, e.g. for			
PT	diagnostic purposes and in development of new anticancer drugs.			
XX	XX			
PS	Disclosure; Fig 5-6; 43pp; Japanese.			
XX	XX			
CC	This sequence represents the human P2X5 protein. The invention relates to			
CC	the P2X5 protein, which is significantly homologous to: (i) the P2X			
CC	family of ATP receptors, and (ii) RP-2 protein which is expressed in			
CC	thymocytes during apoptosis. Transcription of the genes is specifically			
CC	regulated by the tumour-suppressor gene p53. The P2X5 gene is			
CC	specifically expressed in skeletal muscle and has been localised to			
CC	chromosome 22q11, an area where mutation and sequence losses frequently			
CC	occur in rhabdoid sarcomas. The genes may be used for diagnostic purposes			
CC	(e.g. by detecting changes occurring in the gene in sarcomas), using			
CC	probes and primers containing or derived from all or part of the genes.			
CC	The genes may further be used in the development of new anticancer drugs			
XX	XX			
SQ	Sequence 455 AA;			
XX	XX			

Query Match 40.1%; Score 892; DB 2; Length 455;

Best Local Similarity 46.6%; Pred. No. 1.3e-78;
Matches 174; Conservative 55; Mismatches 108; Indels 36; Gaps 5;

QY 12 LLDYKTEK-----WALLAKKGQERDLEPQFSIITLKG 45
DB 13 LFDYKTAFFVAKSKVGLLRVLQIILLVLLWFLIKSYODIDTSQSAAVTKVG 72
QY 46 VSVTQIKELGNRLMDVADFKPPQGENVFFLVTFNLPVPAQVQGRCPHPSVPLANCWD 105
DB 73 VAYTNTMLGERLMDVADFKVPSQGENVFFVVTNLTNPORQICAEERIPDGECS 132
QY 106 EDCPEGEGTHSHGKTCQCV-VFNGTHRTCEIWSGCVPSRPLLAQONFTLFI 164
DB 133 DCHAGESVWAGHGLTKGRCLRVGNSTRGTCEIFAMCPEVTKSMPTDPLKDAESFTISI 192
QY 165 KNTVTFKSNFNSKNALETWPTVFKHCRYPQSPYCPVFRIGDLVAKAGGTFFEDIAL 224
DB 193 KNFIRPKFNSKANVLETDNKHFLKTCFHS-STNLYCPIPRLGSIVRWAGADFODIALK 251
QY 225 GSGVIRVHWDCLDITGSGCWPHYSP-QLQEK-----SYNFRATHWQPCVEART 276
DB 252 GGVIGIYIEWDCDLKAAKCNPHYFNRLDNKHTHSISSGYNFRFARYRDPNGVEFRD 311
QY 277 LKLGIRFDILVTQAGKGLIPTAVTLGTGAALGVVTFCDLLLLYVDREAHFYWRT 336
DB 312 LMKAYGIRFDVIVNGKAKFSIIPVINGSLALMGAGAFCDLVLILIRKSEFYRDK 371
QY 337 KYEAKAPKATAN 349
DB 372 KPEKVRGQKEDAN 384

RESULT 11

ADAE07989
ID ADE07989 standard; protein; 422 AA.
AC ADE07989;
XX
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #144.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376043P.
XX
PA (HYSE-Y) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QH, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR N-PSDB; ADE07078.
XX
XX New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

XX Claim 20; SEQ ID NO 1055; 1177pp; English.
XX
XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 422 AA;

Query Match 37.1%; Score 825.5; DB 7; Length 422;
Best Local Similarity 42.7%; Pred. No. 4.1e-72;
Matches 166; Conservative 63; Mismatches 125; Indels 35; Gaps 7;

QY 20 WALLAKKGQERDLEPQFSIITLKGVSVTQIKELGNRLMDVADFKPPQGENVFFLVN 79
DB 46 WYFWEKGTQETD-SVVSSTTKVKGAVTNTSKLGFINDVADIVIPAQENSILFVMTN 104
QY 80 FLVTPAQVQGRCPHPSVPLANCWDEDCPEGEGTHSHGKTCQCVFNGTHRTCEIWS 139
DB 105 VILTMNQTQGLCPETDATTV-CKSDASCTAGSAGTHSGVSTGRCAFNAGSVKTCVAA 163
QY 140 WCPVESGV-VPSRPLLAQONFTLFIKNTVTFKSNFNSKNALETWPTVFKHCRYPQF 198
DB 164 WCPVEDDTHVQPAFLKAAENFTLLVKNINWPKNFNKRNLFPNITTYLKSLYDAKT 223
QY 199 SPYCPVFRIGDLVAKAGGTFFEDIALLGSGVIRVHWDCLDITGSGCWPHYSPQLOE--- 255
DB 224 DPFCIFRLGKIVENAGHSFQDMAVEGGIMGIVQVWDCNLDRAASLCLPRYSFRELDRD 283
QY 256 -----KSNFRATHWQPCVEARTLLKLYGIRFDILVTQAGKGLIPTAVTLGTGA 309
DB 284 VEHNVSFGYNFRFARYRDLAGNEQRTLIKAYGIRFDIIVFGKAGKFDIIPITMINIGSL 343
QY 310 AWLGVTFFCDLLLLYVDREAHFYWRTKYEEAKAPKATANSVWRELALASQARLAECLE 369
DB 344 ALLGMATVLCDIIVLYCMKRLYREKXKYVEDYEQVGPS-W----- 385
QY 370 SSAPAPTATAA---GSQTQTPGWPSPSSD 395
DB 386 --PPAGTGLSLGCGSPGRGVPWGGPSAE 412

RESULT 12

ADAF76897
ID ADF76897 standard; protein; 422 AA.
XX
XX ADF76897;
AC
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SeqID 572.
XX
XX human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
XX WO2003072035-A5.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005241.
XX
XX 22-FEB-2002; 2002US-0359461P.
PR

XX PA (GETH) GENENTECH INC.
 XX PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 XX PI Williams PM, Wood WI, Wu TD;
 XX DR N-PSDB; ADF76896.
 XX DR WPI; 2003-721702/68.
 XX PT New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.
 XX PS Claim 10; SEQ ID NO 572; 918pp; English.
 XX CC This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neuropeptides and hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytosolic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.
 XX SQ Sequence 422 AA;

Query Match 36.9%; Score 822; DB 7; Length 422;
 Best Local Similarity 40.3%; Pred. No. 9.2e-72;
 Matches 173; Conservative 60; Mismatches 120; Indels 76; Gaps 9;

QY 12 LLDYKTEK-----WALLAKGYQERDLEPQSIITKLG 45
 DB 13 LFDYKTEKYIAKNKKVGLLYRLLOASTLAYLVVWVFLIKKGQDVTSLQSAVITKVG 72
 QY 46 VSVTQIKELGNRLMDVADVFKPKQGENVFELVFNLTVPQVQGRCPHEPSVPLANCWD 105
 DB 73 VAFNTSDLGRIWDVADYVIPAQGENVFVFNLTVPNQVNQVCAENEGIPDGACSKD 132
 QY 106 EDCPEGEGTHSHGVKTCQCVFNGTHR-TCEIWSWCPVSGVPSRPLLAQAQNTFLFI 164
 DB 133 SDCHAGEAVTAGNGVTKGRCLRGNLARGTCEIFAWCPLTSSRPEEPFLKEAEDFTIFI 192
 QY 165 KNTVTSKFNFSKNALETWDPYFKHCYEPQSPYCPVFRIGDLVAKAGTFEDLALL 224
 DB 193 KNHIRFPKFNKNNVMDVKDRSLKSCHEGPK-NHYCPIFRGLSIVRWAGSDFQIALR 251
 QY 225 GGSVGIRVHWDCLDPTGDSGCWPHYSF-QLQEK-----SYNFRATHWEPQVEART 276
 DB 252 GGVIGINTENWCDLKAASECHPYSFGRLDNKLKSVSSGYNFRFARYRDAAGVEPT 311
 QY 277 LKLYGIRPDIIVTQAGKFGILPATIVLTGTAAMLGWVTFPCDLLLLYVDREAHFYWRT 336
 DB 312 LMKYGIIRDVMVNGK-----AFFCDLVLLYIKKREFFYRDK 349
 QY 337 KYEEAKAPKATANSVWRLEALASQARLAECRLRSSAPA-----PTATAAGSQ 383
 DB 350 KYEEVRLGLEDSSQEADE---ASGLGLEQL---TSGPGLLGWPEQQLQEPPEAKRGSSS 404
 QY 384 TOTPGWPCP 392

Db 405 QKGGSGVCP 413

RESULT 13

ID ADP49181

XX ADP49181 standard; protein; 422 AA.

XX AC ADP49181;

XX DT 26-AUG-2004 (first entry)

XX DE Human P2X5 purinergic receptor protein sequence for odour modulation.

XX KW odour sensitivity; P2X purinergic receptor; P2Y purinergic receptor;

XX KW signal transduction pathway; olfactory signalling; micro-array.

XX OS Homo sapiens.

XX PN WO2004047749-A2.

XX PD 10-JUN-2004.

XX PF 21-NOV-2003; 2003WO-US037389.

XX PR 21-NOV-2002; 2002US-0428140P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PI Lucero M, Hegg C;

XX DR WPI; 2004-460642/43.

XX PT Modulating odor sensitivity in a subject, comprises administering a
 PT composition comprising an agonist or antagonist of P2X or P2Y purinergic
 PT receptor to the subject.
 XX PS Disclosure; SEQ ID NO 10; 108pp; English.
 XX CC The invention relates to a method of modulating (M1) odour sensitivity in
 CC a subject, by administering a composition which is an agonist or
 CC antagonist of a P2X or P2Y purinergic receptor. (M1) is useful for
 CC modulating odour sensitivity in a subject (claimed). The compositions
 CC used for modulating odour sensitivity in a subject are useful for
 CC studying the signal transduction pathways related to olfactory signaling.
 CC The compositions are also useful as reagents in micro-arrays or as
 CC reagents to probe or analyze existing micro-arrays. This sequence
 CC corresponds to the human P2X5 protein sequence.

Sequence 422 AA;

Query Match 36.9%; Score 822; DB 8; Length 422;

Best Local Similarity 40.3%; Pred. No. 9.2e-72;

Matches 173; Conservative 60; Mismatches 120; Indels 76; Gaps 9;

QY 12 LLDYKTEK-----WALLAKGYQERDLEPQSIITKLG 45

DB 13 LFDYKTEKYIAKNKKVGLLYRLLOASTLAYLVVWVFLIKKGQDVTSLQSAVITKVG 72

QY 46 VSVTQIKELGNRLMDVADVFKPKQGENVFELVFNLTVPQVQGRCPHEPSVPLANCWD 105

DB 73 VAFNTSDLGRIWDVADYVIPAQGENVFVFNLTVPNQVNQVCAENEGIPDGACSKD 132

QY 106 EDCPEGEGTHSHGVKTCQCVFNGTHR-TCEIWSWCPVSGVPSRPLLAQAQNTFLFI 164

DB 133 SDCHAGEAVTAGNGVTKGRCLRGNLARGTCEIFAWCPLTSSRPEEPFLKEAEDFTIFI 192

QY 165 KNTVTSKFNFSKNALETWDPYFKHCYEPQSPYCPVFRIGDLVAKAGTFEDLALL 224

DB 193 KNHIRFPKFNKNNVMDVKDRSLKSCHEGPK-NHYCPIFRGLSIVRWAGSDFQIALR 251

QY 225 GGSVGIRVHWDCLDPTGDSGCWPHYSF-QLQEK-----SYNFRATHWEPQVEART 276

DB 252 GGVIGINTENWCDLKAASECHPYSFGRLDNKLKSVSSGYNFRFARYRDAAGVEPT 311

QY 277 LKLYGIRPDIIVTQAGKFGILPATIVLTGTAAMLGWVTFPCDLLLLYVDREAHFYWRT 336

DB 312 LMKYGIIRDVMVNGK-----AFFCDLVLLYIKKREFFYRDK 349

QY 337 KYEEAKAPKATANSVWRLEALASQARLAECRLRSSAPA-----PTATAAGSQ 383

DB 350 KYEEVRLGLEDSSQEADE---ASGLGLEQL---TSGPGLLGWPEQQLQEPPEAKRGSSS 404

QY 384 TOTPGWPCP 392

Db 252 GGVIIGINIWNCDLKAASECHPHYSFRLDNKLSKSVSSYNFRFARYRDAAVGFRT 311
 QY 277 LLKLYGIRFDILVTQAGKFGLIPTAVTLGTGAAMLGVVTFPCDLLLLLYVDREAHFYWT 336
 Db 312 LMKAGIRFDVWNGK-----AFFCDLVLIYLIKKEFYRDK 349
 QY 337 KYEAKAKATANSVWRELALASQARLAECURRSAPA-----PTATAAGSQ 383
 Db 350 KYEEVRLGLEDSSQEADE---ASGLGLSEQL--TSGPGLGLMPQEQLOPPPEAKRGSS 404
 QY 384 TQTPCWPCCP 392
 Db 405 QKNGSVCP 413

RESULT 14
 AAW47067
 ID AAW47067 standard; protein; 404 AA.
 AC AAW47067;
 XX
 XX 18-MAY-1998 (first entry)
 DT
 DE Human brain P2X-2 receptor polypeptide.
 KW Brain; P2X receptor; treatment; trauma; spinal cord; infection; human;
 KW inflammation; mood disorder.
 OS Homo sapiens.
 XX
 XX WO9741222-A1.
 XX
 XX 06-NOV-1997.
 XX
 XX 30-APR-1996; 96WO-GB001034.
 XX
 XX 30-APR-1996; 96WO-GB001034.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX McHale MT, Tomlinson WJ, Livingstone CD, Carpenter DJ, Yi L;
 XX WPI; 1997-549726/50.
 XX N-PSDB; AAV09308.
 XX
 XX DNA encoding human brain P2X receptors - used to develop products for
 XX treating, e.g. brain or spinal cord traumas, infection, inflammation and
 XX mood disorders.
 XX
 XX Claim 13; Fig 4; 31pp; English.
 XX
 XX This is a human brain P2X-2 receptor polypeptide. The P2X receptor splice
 XX variants (P2X-1, P2X-2 and P2X-3 isoforms) can be recombinantly expressed
 XX by a host cell genetically engineered with a vector containing the
 XX encoding nucleic acids. The receptors can be used to screen for their
 XX antagonists. The products can be used to identify agents which modulate
 XX the activity of the receptors for use in clinical conditions such as
 XX brain stroke, brain or spinal cord traumas, infection and inflammation,
 XX cognitive disorders, epilepsy, affective and mood disorders in general,
 XX including depression, various movement disorders including Parkinson's
 XX disease, Huntingtons Chorea and schizophrenia, as well as those
 XX conditions that are associated with the development of chronic or acute
 XX forms of pain, or cardiac anoxia. The products can also be used for
 XX detection, production of antibodies and production of transgenic animals
 XX as models for mutation and structure/activity relationship evaluations as
 XX well as in drug screening

Sequence 404 AA;

Query Match 36.7%; Score 818; DB 2; Length 404;
 Best Local Similarity 46.8%; Pred. No. 2.1e-71;
 Matches 155; Conservative 57; Mismatches 107; Indels 12; Gaps 4;

QY 19 KWALLAKGYQERDLEPOFSIITKLKGVSVTQIKELGNRLMDVADFVKPOGENVFLVLT 78
 Db 61 RWFVWEKGYQETD-SVSSVTTKVGAVTNTSKLGFRIWDVADYVIPAQEENSLFVMT 119
 QY 79 NELVTPAQOQRCPSHPSPVLANCVWDEDCPEGEGTHSHGVKTCQCQVVFNGTHRTCEIW 138
 Db 120 NVILTNQOGLCPILPATTV-CKSDASCSTAGSAGTHSNGVSTGRCVAFNGSVKTCVA 178
 QY 139 SWCPVESGV-VPSRPELLAQANFTLFIKNTVTFSTFNFNSKSNALWTWDTFYKHCRIYEPQ 197
 Db 179 AWCPEVDDTHVPQAPAFKAAENFTLLVKNINWYKFNFSKENILFNITTTVLKSCIYDAK 238
 QY 198 FSPYCPVFRIGDLVAKAGGTFFDLALGSGSVGIRVHWCDDLTGSGCWPHYSFLOE-- 255
 Db 239 TDFCFIFRLGKIVENAGHSFQDMAVEGIMGIGIQVWDCNLDRAASLCLPRYSFRLDTR 298
 QY 256 -----KSYNFRATATHWHPQGVFEARTLLKLYGIRFDILVTGQAGKFGLIPTAVTLGTG 308
 Db 299 DVEHNVSPGYNFRFAKYVRDLAGNEQRTLIKAYGIRFDIIVFGKAGKFDIITPTMINISG 358
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RESULT 15
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 ID AAW47066 standard; protein; 388 AA.
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 XX AAW47066;
 XX
 XX 18-MAY-1998 (first entry)
 DT
 DE Human brain P2X-1 receptor polypeptide.
 XX
 XX Brain; P2X receptor; treatment; trauma; spinal cord; infection; human;
 XX inflammation; mood disorder.
 OS Homo sapiens.
 XX
 XX WO9741222-A1.
 XX
 XX 06-NOV-1997.
 XX
 XX 30-APR-1996; 96WO-GB001034.
 XX
 XX 30-APR-1996; 96WO-GB001034.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX McHale MT, Tomlinson WJ, Livingstone CD, Carpenter DJ, Yi L;
 XX WPI; 1997-549726/50.
 XX N-PSDB; AAV09307.
 XX
 XX DNA encoding human brain P2X receptors - used to develop products for
 XX treating, e.g. brain or spinal cord traumas, infection, inflammation and
 XX mood disorders.
 XX
 XX Claim 13; Fig 3; 31pp; English.
 XX
 XX This is a human brain P2X-1 receptor polypeptide. The P2X receptor splice
 XX variants (P2X-1, P2X-2 and P2X-3 isoforms) can be recombinantly expressed
 XX by a host cell genetically engineered with a vector containing the
 XX encoding nucleic acids. The receptors can be used to screen for their
 XX antagonists. The products can be used to identify agents which modulate
 XX the activity of the receptors for use in clinical conditions such as
 XX brain stroke, brain or spinal cord traumas, infection and inflammation,
 XX cognitive disorders, epilepsy, affective and mood disorders in general,
 XX including depression, various movement disorders including Parkinson's
 XX disease, Huntingtons Chorea and schizophrenia, as well as those

Db 344 ALLGMATVLCDIIVLYCMKKRLYREKKYK 373

Search completed: November 21, 2004, 15:00:13
Job time : 160 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 12:30:45 ; Search time 8628.1 Seconds
(without alignments)
11373.559 Million cell updates/sec

Title: US-09-820-095B-1
Perfect score: 2693
Sequence: 1 ttgtgactcatgtgcgcg.....aaaaaaaaaaaaaaaaaaaaa 2693

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1508	56.0	2191	3	BC047287 Homo sapi
2	857.8	31.9	1068	5	EX338022 BX338022
3	772.8	28.7	2222	3	AK081308 Mus muscu
4	751	27.9	787	4	BG920544 602782887
5	740.8	27.5	850	8	AQ748500 HS_5540_A
6	737.4	27.4	1022	5	EX359188 EX359188
7	640.6	23.8	682	2	BF529980 602042384
8	584.2	21.7	3383	3	AK054195 Mus muscu
9	576.2	21.4	741	4	BI821165 603035061
10	561	20.8	733	4	BI753477 603026391
11	553	20.5	718	6	CF131935 UI-HF-PQ0
12	552	20.5	552	4	BM963078 UI-E-DW0
13	472.8	17.6	1038	4	BI757011 603028734
14	466.4	17.3	477	2	AW293881 UI-H-BW0
15	450.4	16.7	460	4	BM689096 UI-E-CQ1
16	445.4	16.5	458	1	AI096436 qb59d11.x
17	417.2	15.5	422	4	BM668009 UI-E-DW0
18	371.4	13.8	651	5	BO210100 UI-R-EP0
19	361.4	13.4	637	6	BY728336 BY728336
20	359.4	13.3	612	6	BY724280 BY724280
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22	347	12.9	497	8	AQ266759 RPC111-76
23	338	12.6	1273	5	BO706537 AGENCOURT
24	337.8	12.5	1071	5	BQ894752 AGENCOURT

ALIGNMENTS

RESULT 1
BC047287
LOCUS BC047287 2191 bp mRNA linear HTC 03-MAR-2003
DEFINITION Homo sapiens, purinergic receptor P2X-like 1, orphan receptor,
clone IMAGE:5198937, mRNA.
ACCESSION BC047287 GI:28703829
VERSION BC047287.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2191)
AUTHORS Strausberg R.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcgaps@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
AKhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masillo, C., Maskari, B., Mastrian, S.D., McCloskey, J.C.,
McGowan, C., Pearson, S., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgoun, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 93 Row: i Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4885534
This clone has the following problem: frame shifted.
FEATURES Location/Qualifiers
1. 2191

AW451665 UI-H-BI3-
AJ346205 shr-00001
BG912438 602806756
BM088220 603616838
AI356622 QY16a11.x
AI703080 W481f03.x
BU30885 603587264
BB666031 BB666031
BF076915 226681 MA
BF075096 223878 MA
BE876713 601488278
CD676001 fs30505.Y
BU274793 603532307
BC017458 Homo sapi
CR623433 full-leng
CR613665 full-leng
CR613673 full-leng
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AY416139 Homo sapi
BC006220 Homo sapi
BC016917 Homo sapi

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ORIGIN

Query Match 56.0%; Score 1508; DB 3; Length 2191;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 1520; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 62 ACAGGCTGGGGCTCTCGATTATAAGACGGAGAAAGTGGGCTCTCTCGCCAAAGGC 121
 DB 113 AGAGGCTGCTGAGTTGGGATCGTGCTATGTGGGCTCTCTCGCCAAAGGC 172
 QY 122 TACAGGAGCGGACCTGGAAACCCAGTTTTCATCATACCAAACTCAAGGGGTTTC 181
 DB 173 TACCAGGAGCGGACCTGGAAACCCAGTTTTCATCATACCAAACTCAAGGGGTTTC 232
 QY 182 GTCACATAGATCAAGGAGCTTGGAAACCGGCTGGGATGTGGCCGACTTCGTGAAGCCA 241
 DB 233 GTCACATAGATCAAGGAGCTTGGAAACCGGCTGGGATGTGGCCGACTTCGTGAAGCCA 292
 QY 242 CCTCAGGAGAGAAAGTGTCTCTTGGTGACCAACTTCCCTGTGACGCCAGCCCAAGTT 301
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 QY 482 GTGCCCTCGAGGCCCTGTCTGGCCAGCCAGACCTTCACTGTTTCATCAAAAACACA 541
 DB 533 GTGCCCTCGAGGCCCTGTCTGGCCAGCCAGACCTTCACTGTTTCATCAAAAACACA 592
 QY 542 GTCACCTTCAGCAAGTTCACATCTCTAAGTCCAAATGCTTGGAGACCTGGGACCCACC 601
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 QY 722 GTAGGCATCAGAGTTCACTGGGATGTGACCTGGACACCGGGACCTGGCTCTGGCT 781
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 QY 1082 GCCAATCTGTGTGGAGGAGCTGGCCCTTGCATCCCAAGCCGCTGCGCGAGTGGCTC 1141
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 QY 1142 AGACGGAGCTCAGACACCTGCACCCACGGCCACTGTGCTGGGAGTCAAGACACCA 1201
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 DB 1613 CTCCTCCAGTGTCTGTCTCCAGTGTCTTCTAGCAGAGTA 1652

RESULT 2
BX338022/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX338022 1068 bp mRNA linear EST 08-APR-2004
 BX338022 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS01054YAL2 3-PRIME, mRNA sequence.
 BX338022
 BX338022.2 GI:46283043
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1068)
 Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30346991.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 10471.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSODI054B6A9NP1&c=10471.f>.
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 /clones="CSODI054YA12"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
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 /note="First strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Query Match 31.9%; Score 857.8; DB 5; Length 1068;
 Best Local Similarity 94.6%; Pred. No. 9.8e-195;
 Matches 919; Conservative 15; Mismatches 32; Indels 5; Gaps 5;

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QY	2429	CTGCACCTCGAGGCTCAGTAAAAATGCTCGGGGTCCCTGTGCTCTCAAATCTCCAGAGC	2488

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Okazaki, Y., Saio, R., Saich, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, I., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES

source

1. .2222
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM,DB:C130003C22"
/db_xref="taxon:10090"
/clone="C130003C22"
/tissue_type="head"
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/note="purinergic receptor P2X-like 1, orphan receptor (MGD|MGF:1337113, GB|NM_011028, evidence: BLASTN, 100%, match=801)
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misc_feature

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Best Local Similarity 75.9%; Pred. No. 3e-174;
Matches 1011; Conservative 0; Mismatches 307; Indels 14; Gaps 4;

ORIGIN

517 CTTCACTGTTTCATCAAAAACACAGTCACTTCTAGCAAGTTCACTTCTCTAAGTCCAA 576
596 CTTGACACTTTCATCAAAAATACCTGTAACTTCTAGCAAGTTCACTTCTCTAAGTCCAA 655
577 TGCTTTGAGACCTGGGACCCACCTATTTAAAGCACTTGCCGCTATGAACACCAATTCAG 636
656 TGCTTTATTAACCTGGGACACACATATTTCAAGCAATTTCTCTATGATCACTCTCCAG 715
637 CCCCTACTGTCCCGTTCCTCGCATTTGGGACCTCTGTGCAAGGCTGGAGAGACCTTCGA 696
716 TCCGTACTGCCAGTGTTCCTGATCGGGACCTTGTGGCCATGGCTGGAGGGGACTTGA 775
697 GGACCTGGCGTT-GCTGGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATTTGACCTGG 755
776 GGACCTGGCGTTGGCTGGGTGGCTGTGGGCATCAGCATTTCACTGGGATTTGCAACCTGG 835
756 ACACGGGGACTTGGCTGGCTCTACTCTCTTCCAGCTTCCAGCTGAGAGAGAGCTACA 815
836 ACACGAAAGGCTCTGACTGCTGTCCCACTCTCTTCCAGCTGAGAGAGAGGCTACA 895
816 ACTTCAGACAGCCACTCACTGGTGGGAGCAACCGGTGTGGAGCCCGCACCTTGTCTCA 875
896 ACTTCAGACAGCCACTCACTGGTGGGAGCAACCGGTGTGGAGCCCGCACCTTGTCTCA 955
876 AGCTCTATGGAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGAGTTGGGGTCA 935
956 AGCTCTATGGAATCCGCTTTGACATTTCTGTCACTGGGACGAGGAGTTGGGGTCA 1015
936 TCCCAACGGCGTCACTGGGACCGGGGAGCTTGGCTGGGGTGGTCACTTCTTCT 995
1016 TCCCTACGGCCATCACTGGGACGAGGCGGTTGGCTGGGATGGTCACTTCTCTCT 1075
996 GTGACCTGCTACTGTGTATGTGATAGAGAGCCATTTCTTCTGGAGGACAAAGTATG 1055
1076 GTGACCTGCTACTGTATGTGATAGAGAGCGGTTTCTTCTGGAGAGCAAAATATG 1135
1056 AGGAGGCAAGCGGCGGAGCAACCGCACTCTGTGTGGAGGAGTGGCCCTTGCAT 1115
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1116 CCCAAGCGGCTGGCGGAGTCCCTCAGACGGAGCTCAGACCTTCCACCCAGCCACTG 1175
1196 CGCTAACCGTGTACCCAGTCTCTAGGAGTGGTTTGCACCTGC-CCCATGCTGCTG 1254
1176 CTGCTGGAGTCAAGACAGA-----CACCAGATGGCCCTGTCCAAGTTCTGAC 1225
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1226 ACCCACTTGCACACCCATTCCGGGAGCTGTAGCGCTTCCCTGTCTGTGAGAGTTGGGG 1285
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1286 GCTGGGAAGG--GGGGGCGCTGCTGGGATCTCAAGGATGAGGCCCGCAGCATGAGGA 1343
1375 CTTGGGAAGGAGGGGTTCTGGCTTGGGAAATGGAGGACAAAGCTTCAGCGGAGTAG 1434
1344 TTGGGGGTAGAAATCCACCTTGAACCCAGCAGACAGTCCCTCCCTGACTCCACCTT 1403
1435 AGGGAGTTGGATTAATTCGACAGACTCCGAATGCAAGATTCCTCTCTGGTTCACTCAG 1494
1404 GGTAGGGTGTG 1415
1495 AGGGTGGGGTG 1506

RESULT 4

BG820544
LOCUS 602782887F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4933821
DEFINITION 5', mRNA sequence.
ACCESSION BG820544
VERSION BG820544.1 GI:14168131
KEYWORDS EST.

337 GGCTAACTGTGGTTCGACGAGGACTCCCGGAGGGGAGGAGGACACACAGCCACCG 396
416 GGCTAACTGTGGCTGATGAGACTGCCCGAAGGGGAGACCGGGACATACAGCCATGS 475
397 TGTAAGAAACAGCCAGTGTGTGTTCAATGGGACCCAGGACCTGTGAGATCTGGAG 456
476 CATAAAGAACTGGTCAAGTGTGTGTTCAACGGAACCCAGGACCTGTGAGATCTGGAG 535
457 TTGTTGCCCACTGGAGAGTGGCTGTGGCTCTCGAGGCCCTCTGTCGCCAGGCCAGAA 516
536 CTGGTGCCCACTGGAGAGTGGTCTGTGCGCCAGGAGGCCCTCTCTAGCTCAGGCCAAGAA 595

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgaabs@mail.nih.gov
              Tissue Procurement: David N. Louis, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (BLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/BLNL at:
              http://image.llnl.gov
              Plate: LNA10861 row: m column: 22
              High quality sequence stop: 733.

FEATURES    source
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              /tissue_type="anaplastic oligodendroglioma with lp/19q
              loss"
              /lab_host="DH10B (T1 phage-resistant)"
              /clone_lib="NCI CGAP Brn67"
              /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
              Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
              Average insert size 2.3 kb. Constructed by Life
              Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match 27.9%; Score 751; DB 4; Length 787;
Best Local Similarity 98.7%; Pred. No. 4,2e-169;
Matches 757; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1913 GCACCGGTCTTCCAGTGGTAGCCCTTTTGCCATGGAGGTCTGGGAGAGACAGAG 1972
DB 1 GCACCGGTCTTCCAGTGGTAGCCCTTTTGCCATGGAGGTCTGGGAGAGACAGAG 60
QY 1973 GCGCGCAGGCTAAGTGGTGATCATTTGGTTCCTCAGACCTTCATATCCCTCTCGG 2032
DB 61 GCGCGCAGGCTAAGTGGTGATCATTTGGTTCCTCAGACCTTCATATCCCTCTCGG 120
QY 2033 TAACCCCCAGCCCAACCCCTTGAATCTTCTCCAGGCTTCTCGAGACCTCGGGGT 2092
DB 121 TAACCCCCAGCCCAACCCCTTGAATCTTCTCCAGGCTTCTCGAGACCTCGGGGT 180
QY 2093 GGGAGGCTGTGGAGGCTGTACATCTGAATTCATTCAGTCCAGTACATACCTAGGAAG 2152
DB 181 GGGAGGCTGTGGAGGCTGTACATCTGAATTCATTCAGTCCAGTACATACCTAGGAAG 240
QY 2153 CTGCTGGGAGCTCTCGAGGGAGGCCCTGGCTCTGATCCAGGCTGGATGGAGTGGCT 2212
DB 241 CTGCTGGGAGCTCTCGAGGGAGGCCCTGGCTCTGATCCAGGCTGGATGGAGTGGCT 300
QY 2213 GGAAGGAATGTTCCAAACACACACCGAGATCTCCCTCAGGCTGGCCAGGTTTTCAG 2272
DB 301 GGAAGGAATGTTCCAAACACACACCGAGATCTCCCTCAGGCTGGCCAGGTTTTCAG 360
QY 2273 CTGGAATTTCTCTTGTCTCCAGGCGGGCAGGGAATTCATAGTGTCCACCCAGGA 2332
DB 361 CTGGAATTTCTCTTGTCTCCAGGCGGGCAGGGAATTCATAGTGTCCACCCAGGA 420
QY 2333 GCGAAGGGGCTGCTTTCCACCTGTGGTACCTGGTGTATCAGGGCAAGCTGTGGAGGGCCAG 2392
DB 421 GCGAAGGGGCTGCTTTCCACCTGTGGTACCTGGTGTATCAGGGCAAGCTGTGGAGGGCCAG 480
QY 2393 GGGTGGGCTGAGACTGGGCTGACATCTAGAATCACTGCCACTGGAGGCTCAGTAAAA 2452

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Db 481 GGGTGGGCTGAGACTGGGCTGACATCTAGAATCACTGCCACTGGAGGCTCAGTAAAA 540
QY 2453 TGCCTGGGGTCCCGTGCCTCTCAATCTCCAGAGCCATCTCCATGGGGAGGTGGGTCT 2512
Db 541 TGCCTGGGGTCCCGTGCCTCTCAATCTCCAGAGCCATCTCCATGGGGAGGTGGGTCT 600
QY 2513 GAAGGGGCAAGTGGGAGAGCAGGCGCCCTCAGGCTGGGTATCCAGAGGGGGCAGGTG 2572
Db 601 GAAGGGGCAAGTGGGAGAGCAGGCGCCCTCAGGCTGGGTATCCAGAGGGGGCAGGTG 660
QY 2573 CACCTGATTTCTCTTGGGGCCAGAGGAGCTGATGTCATGGGTGGGACAAAGTCACGGAG 2632
Db 661 CACCTGATTTCTCTTGGGGCCAGAGGAGCTGATGTCATGGGTGGGACAAAGTCACGGAG 720
QY 2633 TAAAGCCAGCAAGCCACCAAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA 2679
Db 721 TAAAGCCAGCAAGCTCACCTTAAAAAACAACCAAAAGGCCCCAAAAAAGGAAAAA 767

RESULT 5
LOCUS      AQ748500/C
DEFINITION HS_5540_A2_G07_T7A_RPCI-11 Human Male BAC Library Homo sapiens
ACCESSION  AQ748500
VERSION     AQ748500.1
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1 (bases 1 to 850)
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
              Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
              Hood,L.
              Sequence-tagged connectors: A sequence approach to mapping and
              scanning the human genome
              Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
              99380589
              PUBMED 1049764
              Contact: Mahairas GG, Wallace JC, Hood L
              High Throughput Sequencing Center
              University of Washington
              401 Queen Anne Avenue North, Seattle, WA 98109, USA
              Tel: (206) 616-3618
              Fax: (206) 616-3887
              Email: jwallace@u.washington.edu
              Clones are derived from the human BAC library RPCI-11. For BAC
              library availability, please contact Pieter de Jong
              (pieterdejong.med.buffalo.edu). Clones may be purchased from
              BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
              or from Research Genetics (info@resgen.com). BAC end Web Server:
              http://www.htsc.washington.edu
              Plate: 1116 row: M column: 14
              Seq primer: T7
              Class: BAC ends
              High quality sequence stop: 850.
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                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
                  /clone="Plate=1116 Col=14 Row=M"
                  /sex="male"
                  /clone_lib="RPCI-11 Human Male BAC Library"
                  /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
                  Male blood DNA was isolated from one randomly chosen donor
                  and partially digested with a combination of EcoRI and
                  EcoRI Methylase. Size selected DNA was cloned into the
                  pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 27.5%; Score 740.8; DB 8; Length 850;

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QY 697 GGACCTGGGCTTGTCTGGGCTCTGTAGGCATCAGAGTTCACT-GGGATTGTGACCTGG 755
Db 753 GGACCTGGGCTTGTCTGGGCTCTGTAGGCATCAGAGTTCACTGGGATTGTGACCTGG 812
QY 756 ACACGGGAGCTCTGGCTGTCTGCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACA 815
Db 813 ACACGGGAGCTCTGGCTGTCTGCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACA 872
QY 816 ACTTCAGGACAGCCACTACTCTGGTGGAGCAACCGGGTGTGAGGCCCGCACCCTGTCTCA 875
Db 873 ACTTCAGGACAGCCACTACTCTGGTGGAGCAACCGGGTGTGAGGCCCGCACCCTGTCTC- 930
QY 876 AGCTTATGAATCCGCTTCGACATCTCTGTCCACGGGCGAGGAGGAAAGTTCCGGCTCA 935
Db 931 AGCTTATGAATCCGCTTCG- -MATCTCGTCACGGGMRG- -CAGGGARXTCCGGCTCA 986
QY 936 TCCCC 940
Db 987 YCCAC 991

RESULT 7
LOCUS BF529980
DEFINITION 602042384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179908
5', mRNA sequence.
ACCESSION BF529980
VERSION BF529980.1 GI:11617343
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9490 row: h column: 21
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loss"
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/clone_lib="NCI_CGAP_Brn67"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source
1. 682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4179908"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 23.8%; Score 640.6; DB 2; Length 682;
Best Local Similarity 99.0%; Pred. No. 1.3e-142;
Matches 676; Conservative 0; Mismatches 4; Indels 3; Gaps 3;
QY 648 CCGTGTTCGGGACCTCTGTGGCCAGGCTGGAGGACCTTCGAGGACCTGGCGT 707
Db 1 CCGTGTTCGGGACCTCTGTGGCCAGGCTGGAGGACCTTCGAGGACCTGGCGT 60

QY 708 TGCTGGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATTGTGACCTGGGACCGGGGACT 767
Db 61 GGCTGGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATTGTGACCTGGGACCGGGGACT 120
QY 768 CTGGCTCTGGCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACAATTCAGGACAG 827
Db 121 CTGGCTCTGGCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACAATTCAGGACAG- 179
QY 828 CCACTCACTGGTGGGAGCAACCGGGTGTGAGGCCCGCACCCTGTCTAGCTTATGGAA 887
Db 180 GCACTCACTGGTGGGAGCAACCGGGTGTGAGGCCCGCACCCTGTCTAGCTTATGGAA 239
QY 888 TCCGCTTCGACATCTCTGTCCACGGGCGAGGAGGAAAGTTCCGGGCTCATCCCCACGCGCG 947
Db 240 TCCGCTTCGACATCTCTGTCCACGGGCGAGGAGGAAAGTTCCGGGCTCATCCCCACGCGCG 239
QY 948 TCACACTGGGCGACCGGGGAGCTTGGCTGGGCGTGTCTACCTTTTCTGTGACCTGCTAC 1007
Db 300 TCACACTGGGCGACCGGGGAGCTTGGCTGGGCGTGTCTACCTTTTCTGTGACCTGCTAC 359
QY 1008 TGCTGTATGTGGATAGAGAGCCCAATTTCTACCTGGAGGACAAAGTATGAGGAGGCCAAGG 1067
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QY 1128 TGGCCGAGTGCCTCAGACGGGCTCAGACCTGCACCCGAGGAGCTGGTGTGGGAGTC 1187
Db 480 TGGCCGAGTGCCTCAGACGGGCTCAGACCTGCACCCGAGGAGCTGGTGTGGGAGTC 539
QY 1188 AGACACAGACACCGAGGATGGCCCTGTCCAAAGTTCTGACACCCCACTTGCACACCCATTCCG 1247
Db 540 AGACACAGACACCGAGGATGGCCCTGTCCAAAGTTCTGACACCCCACTTGCACACCCATTCCG 599
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Db 600 GAGGCTGTAGCCGTTCCCTGTGTGTGAGTGGGGCTGGAGGAGGGGGGGCCCTGC 658
QY 1308 CTGGGATCTCAAGGATGAGGCC 1330
Db 659 CT-GGGATCTCAAGGATGAGGCC 680

AK054195 3383 bp mRNA linear HTC 03-APR-2004
Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
full-length enriched library, clone:E230027A21 product:purinergic
receptor P2X-like 1, orphan receptor, full insert sequence.
AK054195
VERSION AK054195.1 GI:26096228
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carrinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493374
MEDLINE
11042159
PUBMED
REFERENCE 3

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE 3

QY 1117 CCAAGCCGACTGGCGAGTCCCTCAGACGGAGCTCAGACCTGCACCCACGGCCACTGTC 1176
 Db 1163 CCTAACCTGTATCCCAAGTCTCCTAGAGTGGTTGCACCTGC-CCCATGTCTGTCTGC 1221
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 QY 1405 GTAGGGTCTG 1415
 Db 1462 GGGGTGGGTG 1472

RESULT 9
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 mRNA sequence.
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11438 row: j column: 15
 High quality sequence stop: 699.
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 /clone_lib="NTH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector:
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 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 C21. Note: this is a NIH_MGC Library."

FEATURES source

BI821165 741 bp mRNA linear EST 04-OCT-2001
 LOCUS 741 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603035061F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176046 5',
 mRNA sequence.
 ACCESSION BI821165
 VERSION BI821165.1 GI:15932715
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11438 row: j column: 15
 High quality sequence stop: 699.
 Location/Qualifiers
 1..741
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5176046"
 /lab_host="DH10B"
 /clone_lib="NTH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector:
 PCMV-SPORE5; Site:1; NotI; Site:2; EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 C21. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.4%; Score 576.2; DB 4; Length 741;
 Best Local Similarity 99.3%; Pred. No. 4e-127;
 Matches 589; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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 QY 157 CATCACAAACTCAAGGGGTTTCCGCTCACTCAGATCAAGGAGCTTGGAAACCGGCTGTG 216
 Db 209 CATCACAAACTCAAGGGGTTTCCGCTCACTCAGATCAAGGAGCTTGGAAACCGGCTGTG 268
 QY 217 GGATGGCGGACTTCGTGAAGCCACTCAGGAGAGAGAGCTTCTTCTTGGTGACCAA 276
 Db 269 GGATGGCGGACTTCGTGAAGCCACTCAGGAGAGAGAGCTTCTTCTTGGTGACCAA 328
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 Db 329 CTTCTTGTGACGCCGCCCAAGTTTCAGGCGCAGATGCCAGAGACACCCGCTCCGTCACCT 388
 QY 337 GGCTAACTGCTGGTGCAGGAGACTGCCCGGAGGGAGGGAGGACACACAGCCACGG 396
 Db 389 GGCTAACTGCTGGTGCAGGAGACTGCCCGGAGGGAGGGAGGACACACAGCCACGG 448
 QY 397 TGTAAAAACAGGCCAGTGTGTGTTCATATGGGACCCACAGACCTGTGAGATCTGGAG 456
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 Db 629 ATGCCCTTGAGACCTCGGACCCCACTATTTAAAGCACTGCCTATGAACACCAATTCA 688
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 mRNA sequence.
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 VERSION BI753477.1 GI:15745055
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11492 row: f column: 24
 High quality sequence stop: 719.
 Location/Qualifiers

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1. 733
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/clone="IMAGE:5196695"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not I; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 20.8%; Score 561; DB 4; Length 733;
Best Local Similarity 82.9%; Pred. No. 1.8e-123;
Matches 719; Conservative 0; Mismatches 0; Indels 148; Gaps 1;

QY 2 TGCTGACTATGTCGCCGACCTAGCAGGAGCTGGCAGCATGGCTCCCGAGGGCTAGC 61
DB 14 TGCTGACTATGTCGCCGACCTAGCAGGAGCTGGCAGCATGGCTCCCGAGGGCTAGC 73

QY 62 ACAGCTGGGGCTCTGGATTATAAGACGAGAGTGGGCTCTCTCGCCAAAAGGC 121
DB 74 ACAGCTGGGGCTCTGGATTATAAGACGAGAGTGGGCTCTCTCGCCAAAAGGC 133

QY 122 TACGAGAGCGGACCTGGAAACCCAGTTTTCATCATACCAAACTCAAGGGTTTCC 181
DB 134 TACGAGAGCGGACCTGGAAACCCAGTTTTCATCATACCAAACTCAAGGGTTTCC 193

QY 182 GTCACTCAGTCAAGGAGCTGGAAACCCGCTGGGATGTGGCGACTTCGTGAAGCCA 241
DB 194 GTCACTCAGTCAAGGAGCTGGAAACCCGCTGGGATGTGGCGACTTCGTGAAGCCA 253

QY 242 CCTCAGGAGAGAACGTGTTCTTCTTGTTGACCAACTTCCTGTGACGCCAGCCCAAGTT 301
DB 254 CCTCA----- 258

QY 302 CAGGCAGATCCAGAGACCCCTCGTCCACTGGCTAACTGCTGGTTCGACGAGAC 361
DB 259 ----- 258

QY 362 TGCCCCGAAGGGAGGAGGCACACAGCCACCGTGTAAACACAGGCCAGTGTGTGGTG 421
DB 259 -----GGTGTAAACACAGGCCAGTGTGTGGTG 285

QY 422 TTCAATGGGACCCACAGAACCTGTGAGATCTGGAGTTGGTGCCCACTGGAGAGTGGCGTT 481
DB 286 TTCAATGGGACCCACAGAACCTGTGAGATCTGGAGTTGGTGCCCACTGGAGAGTGGCGTT 345

QY 482 GTGCCCTCAGGCGCCCTCTGCGCCAGCCAGCAACTTCACACTGTTTCATCAAAAACACA 541
DB 346 GTGCCCTCAGGCGCCCTCTGCGCCAGCCAGCAACTTCACACTGTTTCATCAAAAACACA 405

QY 542 GTCACCTTCAGCAAGTTCACACTTCTTAAGTCCAAATGCCCTTGGAGACTGGGACCCCAAC 601
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QY 602 TATTTTAGCACTCCGCTATGACCAACAATTCAGCCCTACTCTCCCGTGTTCCGCAAT 661
DB 466 TATTTTAGCACTCCGCTATGACCAACAATTCAGCCCTACTCTCCCGTGTTCCGCAAT 525

QY 662 GGGACCTCTGCGGCAAGCTGGAGGACCTTCGAGGACCTGGCGTTGCTGGGTGGCTCT 721
DB 526 GGGACCTCTGCGGCAAGCTGGAGGACCTTCGAGGACCTGGCGTTGCTGGGTGGCTCT 585

QY 722 GTAGCATCAGATTCACTGGATGTGACCTGACACCGGGGACTCTGCTCTGCGCT 781
DB 586 GTAGCATCAGATTCACTGGATGTGACCTGACACCGGGGACTCTGCTCTGCGCT 645

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QY 782 CACTACTCTTCCAGCTGCAGGAGAGCTACAACTTCAGGACAGCACTCACTGCTGG 841
DB 646 CACTACTCTTCCAGCTGCAGGAGAGCTACAACTTCAGGACAGCACTCACTGCTGG 705

QY 842 GAGCAACCGGGTGTGGAGCCCGCACC 868
DB 706 GAGCAACCGGGTGTGGAGCCCGCACC 732

CFI31935 718 bp mRNA linear EST 05-AUG-2003
UI-HF-PQ0-aws-m-11-0-UI.r1 NIH_MGC_215 Homo sapiens cDNA clone
IMAGE:30553930 5', mRNA sequence.

CFI31935
CFI31935.1 GI:33214691
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
Ronald, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5.
Location/Qualifiers
1. 718
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_MGC_215"
/notes="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CATAAGGCCA. Tissue was provided by Mary Hendrix."

FEATURES
source
Query Match 20.5%; Score 553; DB 6; Length 718;
Best Local Similarity 99.5%; Pred. No. 1.5e-121;
Matches 564; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 97 GTGGGCTCTCTCTCGCAAAAAGGCTACAGAGCGGACCTGGAAACCCAGTTTCCAT 156
DB 153 GTGGGCTCTCTCTCGCAAAAAGGCTACAGAGCGGACCTGGAAACCCAGTTTCCAT 212

ORIGIN
Query Match 20.5%; Score 553; DB 6; Length 718;
Best Local Similarity 99.5%; Pred. No. 1.5e-121;
Matches 564; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 217 GATGTGGCGGCTTCTGTAAGCCACTCAGGAGAGAACGTGTTCTTCTTGGTGACCAA 276
Db 273 GATGTGGCGGCTTCTGTAAGCCACTCAGGAGAGAACGTGTTCTTCTTGGTGACCAA 332
QY 277 CTTCTCTGTGAGCGCCAGCCCAAGTTTCAGGGCAGATGCCAGAGCACCGTCCGTCCTCACT 336
Db 333 CTTCTCTGTGAGCGCCAGCCCAAGTTTCAGGGCAGATGCCAGAGCACCGTCCGTCCTCACT 392
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Db 393 GCGTAACCTCTGGTTCGACGAGACTGCCCGAAGGGAGGAGCACACACAGCCACGG 452
QY 397 TGTAAAAACAGCCAGTGTGTTGTTCAATGGGACCCACAGGACCTGTGATCTGGAG 456
Db 453 TGTAAAAACAGCCAGTGTGTTGTTCAATGGGACCCACAGGACCTGTGATCTGGAG 512
QY 457 TTGGTGCCAGTGGAGTGGGTTGTGCTTCGAGGCCCTGTGCGCCAGGCCAGAA 516
Db 513 TTGGTGCCAGTGGAGTGGGTTGTGCTTCGAGGCCCTGTGCGCCAGGCCAGAA 572
QY 517 CTTCACTGTTCATCAAAAACACAGTCACTTCAGAGTTCACTTCTTAAGTCAA 576
Db 573 CTTCACTGTTCATCAAAAACACAGTCACTTCAGAGTTCACTTCTTAAGTCAA 632
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QY 637 CCCCTACTGTCCCGTGTCCGCAATTGG 663
Db 692 CCCCTACTGTCCCGTGTCCGCAATTGG 718

RESULT 12
BM696978
LOCUS
DEFINITION
UI-E-DW0-agl-f-08-0-UI-r1 UI-E-DW0 Homo sapiens cdna clone
ACCESSION
BM696978
VERSION
BM696978.1 GI:19010236
KEYWORDS
EST.
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 552)
AUTHORS
Ronald, M.F., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
1..552
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/clone_lib="UI-E-DW0"
/notes="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-DW0 is a cDNA library containing the following
tissue(s): lens. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pRTT3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CGATTACGGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 20.5%; Score 552; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 2.5e-121;
Matches 552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1904 AGTTATGAGACCGGCTGCTTCCAGTGTAGCCCTTTTGGCATGGAGTCTGGGAGAG 1963
Db 1 AGTTATGAGACCGGCTGCTTCCAGTGTAGCCCTTTTGGCATGGAGTCTGGGAGAG 60
QY 1964 AGAGCAGAGGCGGCGAGGCTAAAGTTGGTGATCATTTGGGTTCTTCAGGACCTTCTATATC 2023
Db 61 AGAGCAGAGGCGGCGAGGCTAAAGTTGGTGATCATTTGGGTTCTTCAGGACCTTCTATATC 120
QY 2024 CTTCTCGGTAAACCCCGCCAGCCCAACCTTGAATTTCTCCAGGCTTCTGAGAGC 2083
Db 121 CTTCTCGGTAAACCCCGCCAGCCCAACCTTGAATTTCTTCCTCAGGCTTCTGAGAGC 180
QY 2084 CTTGGGGGTGGGAGGCTGTGGGAGGCTGTACATCTGAAATTCATTTCAAGTCCAAAGTCATA 2143
Db 181 CTTGGGGGTGGGAGGCTGTGGGAGGCTGTACATCTGAAATTCATTTCAAGTCCAAAGTCATA 240
QY 2144 CTTAGGAGCTGTCTGGGAGCTGTCTGAGGAGGCGCTGGCTCTGATCCAGGCTGGAT 2203
Db 241 CTTAGGAGCTGTCTGGGAGCTGTCTGAGGAGGCGCTGGCTCTGATCCAGGCTGGAT 300
QY 2204 GGAGTGGCTGGAAGGAATGTTCCAAACACACCCAGAGATCTCCCTCAGGCTGGCCAG 2263
Db 301 GGAGTGGCTGGAAGGAATGTTCCAAACACACCCAGAGATCTCCCTCAGGCTGGCCAG 360
QY 2264 GTTTTCAGCTGGAATTTCTCTTGGTCCCGAGGCGGGGAGGGAATTTCTAAGTGTCCA 2323
Db 361 GTTTTCAGCTGGAATTTCTCTTGGTCCCGAGGCGGGGAGGGAATTTCTAAGTGTCCA 420
QY 2324 CCCCAGGAGGCGAAGGGCTGCTTTCCACTGTGGTACCTGTGTGATCAGGCGAAGTGTG 2383
Db 421 CCCCAGGAGGCGAAGGGCTGCTTTCCACTGTGGTACCTGTGTGATCAGGCGAAGTGTG 480
QY 2384 GAGGCGCAGGGGTGGGGCTGAGACTGGGCTGACATCTAGAAATCACCTGCCACCTGGAGCC 2443
Db 481 GAGGCGCAGGGGTGGGGCTGAGACTGGGCTGACATCTAGAAATCACCTGCCACCTGGAGCC 540
QY 2444 TCAGTAAATGC 2455
Db 541 TCAGTAAATGC 552

RESULT 13
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DEFINITION
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BI757011 1038 bp mRNA linear EST 25-SEP-2001
603028734F1 NIH_MGC_114 Homo sapiens cdna clone IMAGE:5198937 5',

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mRNA sequence.
BI757011.1 GI:15748589
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM11498 row: d column: 10
High quality sequence stop: 698.
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            /clone_lib="NIH_MGC_114"
            /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
            male brains, age range 23-27 yo. Library is oligo-dT
            primed and directionally cloned (EcoRV site is destroyed
            upon cloning). Average insert size 1.5 kb, insert size
            range 1-3 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 019. Note:
            this is a NIH_MGC Library."
ORIGIN
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    Best Local Similarity 92.2%; Pred. No. 3e-102;
    Matches 588; Conservative 0; Mismatches 37; Indels 13; Gaps 8;
QY 62 ACAGCTGGGGCTCTCGATTATAGACGGAGAGTGGGCTCTCTCGCAAAAAGGC 121
Db 112 AGAGCTGCTCAGTTGGGATCGGTCTATGTGGTGGGCTCTCTCGCAAAAAGGC 171
QY 122 TACCAGGACGGGACCTGGAAACCCAGTTTCCATCATCAACCAACTCAAAAGGGTTTC 181
Db 172 TACCAGGACGGGACCTGGAAACCCAGTTTCCATCATCAACCAACTCAAAAGGGTTTC 231
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Db 292 CCTCAGGAGAGACGTTCTTCTTG-GTGAGTGACCAACTCTCTGTGACGCCAGCCCAAGT 351
QY 301 TCAGGACAGATGCCAGAGCACCGCTCGTCCCACTGGCTTAATCTGTGGTGCACAGGCA 360
Db 352 TCAGGACAGATGCCAGAGCACCGCTCGTCCCACTGGCTTAATCTGTGGTGCACAGGCA 411
QY 361 CTGCCCCAGGAGGAGGAGGACACACAGCAGCGGTGTAACACAGGCGAGTGTGTGGT 420
Db 412 CTGCCCCAGGAGGAGGAGGAGGACACACAGCAGCGGTGTAACACAGGCGAGTGTGTGGT 471
QY 421 GTTCAATGGGACCCACAGGACCTGTGAGATCTGAGTGTGTGGCCAGTGAGAGTGGCGT 480
Db 472 GTTCAATGGGACCCACAGGACCTGTGAGATCTGAGTGTGTGGCCAGTGAGAGTGGCG- 530

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477 bp mRNA linear EST 16-JAN-2000

UI-H-BWQ-ain-e-06-0-UI-s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone

IMAGE:2729939 3', mRNA sequence.

AW293881

AW293881

AW293881.1 GI:6700517

EST.

Source

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP clone distribution information can be found through the

I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/sbrp/image/image.html

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1..477

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2729939"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Sub6"

/note="Vector: pT7T3P-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub6

is a subtracted library derived from BW, which consists of

a mixture of four normalized libraries: NCI CGAP Brn50,

NCI CGAP Lul3, NCI CGAP Ovi8, GBC1. The NCI CGAP Sub6

library had 7 million recombinants. A single-stranded DNA

preparation of BW was used as a tracer in a subtractive

hybridization with a driver comprising: the IMAGE pool

(NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683,

3798-3803 (IMAGE Clonoids 1322376-1323911,

1456008-1456775, 1502855-1502855); NCI CGAP Kid5 pool 1

LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids

1323912-1325831, 1471368-1472903, 1492104-1493255);

NCI CGAP Lul3 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE

Clonoids 1414920-1417991, 1520904-1522439); NCI CGAP_GC4

pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE

Clonoids 1257096-1258631, 1469064-1470983,

1475592-1476743); NCI CGAP Pr22 pool 1 LLAM 2457-2459,

2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759,

COMMENT

FEATURES source

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/db_xref="taxon:9606"
/clone="UI-E-CQ1-act-a-11-0-UI"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phase resistant)"
/clone_lib="UI-E-CQ1"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-CQ1 is a normalized cDNA library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA,
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CCATTAAAGTG. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."

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	Query Match	16.7%	Score 450.4	DB 4	Length 460	
	Best Local Similarity	99.8%	Pred. No. 66-97			
	Matches 451	Conservative 0	Mismatches 1	Indels 0	Gaps 0	
QY	2070	GCCTTCCTGAGAGCCCTCGGGCTGGAGGCTGTGGAGGCTGTACATCTGAATTCACATT	2129			
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QY	2130	CAGTCCAAAGTCATACCTAGGAAGCTGTCTGGSCAGCTGCTCAGGGAGGCCCTGGGCTGTG	2189			
DB	69	CAGTCCAAAGTCATACCTAGGAAGCTGTCTGGSCAGCTGCTCAGGGAGGCCCTGGGCTGTG	128			

QY	2190	ATCCCAGGCTGGATGGAGTGGCTGGAAGAAATGGTTCCAAACAAACACACACCGAGATCTCC	2249
Db	129	ATCCCAGGCTGGATGGAGTGGCTGGAAGAAATGGTTCCAAACAAACACACCGAGATCTCC	188
QY	2250	CTCAGGCTGGCCAGSTTTTTCAGCTGGAAATCTCTCTTGTCCAGGGCGGGCAGGGA	2309
Db	189	CTCAGGCTGGCCAGSTTTTTCAGCTGGAAATCTCTCTTGTGTCCAGGGCGGGCAGGGA	248
QY	2310	ATTCTAAGTGTCCACCCAGGAGGCAAGGGGCTGCTTTCACCTGTGGGTACTCGTGAT	2369
Db	249	ATTCTAAGTGTCCACCCAGGAGGCAAGGGGCTGCTTTCACCTGTGGGTACTCGTGAT	308
QY	2370	CAGGCGAAGCTCTGGAGGCCAGGGTGGGGCTGAGCTGGGTGCACATCTAGAATCACC	2429
Db	309	CAGGCGAAGCTCTGGAGGCCAGGGTGGGGCTGAGCTGGGTGCACATCTAGAATCACC	368
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Sun Nov 28 09:38:14 2004

Qy 2490 ATGTCCATGGGAGGTGGGCTCTGAGGGCGA 2521
| | | | | | | | | | | | | | | | | | | | | |
Db 429 ATGTCCATGGGAGGTGGGCTCTGAGGGTGA 460

Search completed: November 21, 2004, 17:35:05
Job time : 8637.1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 21, 2004, 17:43:16 ; Search time 1331.37 Seconds
(without alignments)
10930.100 Million cell updates/sec

Title: US-09-820-095B-1
Perfect score: 2693
Sequence: 1 ttgtgactcatgtgcgcg.....aaaaaaaaaaaaaaaaaaaaa 2693

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 362788 seqs, 270181610 residues
Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq:
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5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq:
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15: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2693	100.0	2693	10	US-09-820-095-1
2	1592.6	59.1	16449	10	US-09-820-095-3
3	567.4	21.1	569	9	US-09-864-761-9190
4	377	14.0	577	9	US-09-864-761-9695
5	243.6	9.0	1978	15	US-10-172-118-786
6	243.6	9.0	1978	16	US-10-342-887-786
7	239.2	8.9	1389	9	US-09-833-082-1
8	237.6	8.8	1269	18	US-10-305-720-831
9	237.2	8.8	1167	15	US-10-128-558-20
10	237.2	8.8	1167	15	US-10-386-414-18
11	237.2	8.8	2048	16	US-10-386-414-16
12	237.2	8.8	2048	16	US-10-240-425-1468

13	236.6	8.8	2048	16	US-10-187-659A-4	Sequence 4, Appli
14	233.4	8.7	2633	9	US-09-969-347-225	Sequence 225, App
15	233.4	8.7	2643	15	US-10-352-684A-53	Sequence 53, Appl
16	233.4	8.7	2643	16	US-10-641-643-897	Sequence 897, App
17	233.4	8.7	2643	17	US-10-283-975A-285	Sequence 285, App
18	226	8.4	1956	9	US-09-864-864-331	Sequence 331, App
19	226	8.4	1986	17	US-10-283-975A-239	Sequence 239, App
20	215.4	8.0	1831	16	US-10-452-879-3	Sequence 3, Appli
21	213.2	7.9	1380	15	US-10-345-680-12	Sequence 12, Appl
22	213.2	7.9	1389	15	US-10-345-680-10	Sequence 10, Appl
23	212.6	7.9	1639	11	US-09-764-875-307	Sequence 307, App
24	181.4	6.7	1616	16	US-10-336-472-53	Sequence 53, Appl
25	163	6.1	1583	16	US-10-336-472-51	Sequence 51, Appl
26	163	6.1	163	9	US-09-864-761-26100	Sequence 26100, A
27	157.4	5.8	159	9	US-09-864-761-25779	Sequence 25779, A
28	156.4	5.8	51	15	US-10-029-386-646	Sequence 646, App
29	156	5.8	647	13	US-10-027-632-158909	Sequence 158909,
30	156	5.8	647	15	US-10-027-632-158909	Sequence 158909,
31	151	5.6	151	15	US-10-029-386-14351	Sequence 14351, A
32	148.4	5.5	565	9	US-09-864-761-9732	Sequence 9732, Ap
33	146.4	5.4	1926	15	US-10-133-013-149	Sequence 149, App
34	146.4	5.4	440	9	US-09-864-761-2179	Sequence 2179, Ap
35	144.6	5.4	576	9	US-09-864-761-9249	Sequence 9249, Ap
36	140.4	5.2	961	16	US-10-051-874-41	Sequence 41, Appl
37	131.2	4.9	941	11	US-09-764-847-250	Sequence 250, App
38	125.8	4.7	941	14	US-10-092-154-250	Sequence 583, App
39	125.8	4.7	941	14	US-10-092-154-250	Sequence 250, App
40	125.8	4.7	941	14	US-10-092-154-250	Sequence 250, App
41	125.8	4.7	941	14	US-10-092-154-250	Sequence 250, App
42	111	4.1	423	9	US-09-864-864-254	Sequence 254, App
43	108.8	4.0	142	9	US-09-864-761-18920	Sequence 18920, A
44	107.8	4.0	1853	17	US-10-977-231-2	Sequence 2, Appli
45	107.8	4.0	1853	17	US-10-766-978-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-820-095-1
; Sequence 1, Application US/09820095
; Publication No. US20030233668A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001202
; CURRENT APPLICATION NUMBER: US/09/820,095
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Human
US-09-820-095-1

Query Match	100.0%;	Score 2693;	DB 10;	Length 2693;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2693;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy	1	TTGCTGACTCATGTGCGCCGACCTAGCAGAGCTGCGAGCATGGCTCCCGAGGGCTAC	60
Db	1	TTGCTGACTCATGTGCGCCGACCTAGCAGAGCTGCGAGCATGGCTCCCGAGGGCTAC	60
Qy	61	GACAGCTGGGGGCTTCTGGATTATAAGACGAGAGTGGGCTCTCTCGCCCAAAAGG	120
Db	61	GACAGCTGGGGGCTTCTGGATTATAAGACGAGAGTGGGCTCTCTCGCCCAAAAGG	120
Qy	121	CTACGAGGCGGGACCTGGACCCCGAGTTTCCATCATCACCACAACTCAAGGGTTTC	180
Db	121	CTACGAGGCGGGACCTGGACCCCGAGTTTCCATCATCACCACAACTCAAGGGTTTC	180

2341	Db	GCTGCTTTCCACTGTGGTACTGTGGTATCAGGGCAAGCTGTGGAGGGCCAGGGGTGGG	2400
2401	Qy	CTGAGACTGGCTGCATCTAGAATCACTCTGCCACCTGGAGCCTCAGTAAATGCTCTGG	2460
2401	Db	CTGAGACTGGCTGCACTAGATCACTCTGCACCTGGAGCCTCAGTAAATGCTCTGG	2460
2461	Qy	GTCCCTGTGCCTCTCAATCTCCAGAGCCATGTCCATGGGAGGTGGGCTCTGAAGGGCG	2520
2461	Db	GTCCCTGTGCCTCTCAATCTCCAGAGCCATGTCCATGGGAGGTGGGCTCTGAAGGGCG	2520
2521	Qy	AAGTGGGAGAGCAGGGCCCCCTGAGCCTGGGTATCCBAGGAGGGGCAGTGCACCTGAT	2580
2521	Db	AAGTGGGAGAGCAGGGCCCCCTGAGCCTGGGTATCCBAGGAGGGGCAGTGCACCTGAT	2580
2581	Qy	TCTCCTTGGGGCCCAGAGGAAGCTGATGTCTGGCTTGGACAAAGTCACGAGTAAAGCCA	2640
2581	Db	TCTCCTTGGGGCCCAGAGGAAGCTGATGTCTGGCTTGGACAAAGTCACGAGTAAAGCCA	2640
2641	Qy	GCAAAGCCACCAAAAAA	2693
2641	Db	GCAAAGCCACCAAAAAA	2693

RESULT 2

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US-09-820-095-3
; Sequence 3, Application US/09820095
; Publication NO. US2003023668A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001202
; CURRENT APPLICATION NUMBER: US/09/820,095
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16449
; TYPE: DNA
; ORGANISM: Human
US-09-820-095-3

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Query Match.	59.1%;	Score 1592.6;	DB 10;	Length 16449;	
Best Local Similarity	99.7%;	Pred. No. 0;			
Matches 1595;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1053	ATGAGGAGGCCAAGGCCCGAAGCAACCGCCAACTCTGTGTGAGGGAGCTGGCCCTTG	1112		
Db	13246	ATTGCAAGCCAAAGCCCCGAAAGCAACCGCCAACTCTGTGTGAGGGAGCTGGCCCTTG	13305		
QY	1113	CATCCCAAGCCCGACTGGCCGAGTGCTCAGACGGAGCTCAGCACTGCACCCACGGCCA	1172		
Db	13306	CATCCCAAGCCCGACTGGCCGAGTGCTCAGACGGAGCTCAGCACTGCACCCACGGCCA	13365		
QY	1173	CTGCTGCTGGAGTCAGACACAGACACCAGATGGGCCCTGTCCAAGTTCTGCACACCCACT	1232		
Db	13366	CTGCTGCTGGAGTCAGACACAGACACCAGATGGGCCCTGTCCAAGTTCTGCACACCCACT	13425		
QY	1233	TGCCAACCCATTCCGGGAGGCTCTAGCCGTTCCCTGCTGTTGAGAGTTGGGGGCTGGGA	1292		
Db	13426	TGCCAACCCATTCCGGGAGGCTCTAGCCGTTCCCTGCTGTTGAGAGTTGGGGGCTGGGA	13485		
QY	1293	AGGCGGGGCCCTGCTCTGGGGAATCTCAAGATGAGGCCCCAGCATGGAGGATGGGGGTA	1352		
Db	13486	AGGCGGGGCCCTGCTCTGGGGAATCTCAAGATGAGGCCCCAGCATGGAGGATGGGGGTA	13545		
QY	1353	GAATTCCACCCCTGAACCCCCAGACAGACAGTCCCTCCCTGACTCCCACTTGGTAGGGTG	1412		
Db	13546	GAATTCCACCCCTGAACCCCCAGACAGACAGTCCCTCCCTGACTCCCACTTGGTAGGGTG	13605		
QY	1413	CTGCTCTCAGGAGGCCATAGAAAGTCGGCTGTGTTTTGAGACGGCCGACAGAACCTGACCCGT	1472		

13606	Db	CTGGCTTCAGGGAGCCATAGAGTCGGCTGTGTTTTGAGACGGCGACGAACCTGACCCGT	13665
1473	Qy	GGAGACTGGGAGAGCCACGACGGCACCTGTATTGACGGGCTCCGACTGCATGTGSCAGGG	1532
13666	Db	GGAGACTGGGAGAGCCACGACGGCACCTGTATTGACGGGCTCCGACTGCATGTGSCAGGG	13725
1533	Qy	GCCTCTGCTGCGTCTGCGGCGCTGGAGGTCTCTCTCCACGTGCTCTGTGCCAGTGTTCCTA	1592
13726	Db	GCCTCTGCTGCGTCTGCGGCGCTGGAGGTCTCTCTCCACGTGCTCTGTGCCAGTGTTCCTA	13785
1593	Qy	GCAGAGGTATGCTTACCAGCTGTGACGACAGACCCTCTGCTGCTGGGTCTTGCCCTC	1652
13786	Db	GCAGAGGTATGCTTACCAGCTGTGACGACAGACCCTCTGCTGCTGGGTCTTGCCCTC	13845
1653	Qy	CTTCCCCATCTGCACCCCCATCATAGGTAGAGACCCCAACCTCCATCGGTCTTACATGG	1712
13846	Db	CTCCCCCATCTGCACCCCCCATCATAGGTAGAGACCCCAACCTCCATCGGTCTTACATGG	13905
1713	Qy	GGCTGTGACGCTGGAGCCAAAAGCAAGGACAGAAAGAGGAGTGTATGGGAGAGGGGGAAT	1772
13906	Db	GGCTGTGACGCTGGAGCCAAAAGCAAGGAGTGTATGAAGAGGAGTGTATGGGAGAGGGGGAAT	13965
1773	Qy	GTTCAGCTTCTCTGGTGTGTGATGCCCCAGGAGAGTCTTAATCTAGGGAATGGGGTGG	1832
13966	Db	GTTCAGCTTCTCTGGTGTGTGATGCCCCAGGAGAGTCTTAATCTAGGGAATGGGGTGG	14025
1833	Qy	AGTAGGCAGATTAATCCACCTCCCTATCCCCACGGCAAGGGCGGAGCATGTCTCTGGGCC	1892
14026	Db	AGTAGGCAGATTAATCCACCTCCCTATCCCCACGGCAAGGGCGGAGCATGTCTCTGGGCC	14085
1893	Qy	CACACCTGCTTAGTTTATGAGGACCGGCTGCTTCCAGTGGTAGGCCCTTTTGCCATGGAG	1952
14086	Db	CACACCTGCTTAGTTTATGAGGACCGGCTGCTTCCAGTGGTAGGCCCTTTTGCCATGGAG	14145
1953	Qy	GTCTGGGAGAGAGAGAGGCGCGCAGGGCTAAGTTGGTGTATCATTTGGGTCTTTCAGGA	2012
14146	Db	GTCTGGGAGAGAGAGAGGCGCGCAGGGCTAAGTTGGTGTATCATTTGGGTCTTTCAGGA	14205
2013	Qy	CTTTCTATATCCCTCTCTGGTAAACCCCCACGCCCCAACCCCTTGGAACTCTTCTCCAGGC	2072
14206	Db	CTTTCTATATCCCTCTCTGGTAAACCCCCACGCCCCAACCCCTTGGAACTCTTCTCCAGGC	14265
2073	Qy	TTCTCTAGAGCCCTGGGGTGGAGGCTGTGGAGGCTGTACATCTGAAAATTCATTCTCAG	2132
14266	Db	TTCTCTAGAGCCCTGGGGTGGAGGCTGTGGAGGCTGTACATCTGAAAATTCATTCTCAG	14325
2133	Qy	TCCNAGTCTATAGTAAGCTGCTGGGACGCTGCTCGAGGGAGGCCCTGGCTCTGATC	2192
14326	Db	TCCNAGTCTATAGTAAGCTGCTGGGACGCTGCTCGAGGGAGGCCCTGGCTCTGATC	14385
2193	Qy	CCAGGTGATGAGTGGCTGGAAGGAATGGTTCCAAACAAACACACCGAGATCTCCCTC	2252
14386	Db	CCAGGTGATGAGTGGCTGGAAGGAATGGTTCCAAACAAACACACCGAGATCTCCCTC	14445
2253	Qy	AGGTGGCCAGGTTTTTGACGTGGAAATTTCTCTCTTTGTTCCAGGGCGGGGACGAGGAAT	2312
14446	Db	AGGTGGCCAGGTTTTTGACGTGGAAATTTCTCTCTTTGTTCCAGGGCGGGGACGAGGAAT	14505
2313	Qy	CTAAGTGTCCACCCACGAGGAGCAAGGGCTGCTTTTCCACTGTGGGTACCTGGTGATCAG	2372
14506	Db	CTAAGTGTCCACCCACGAGGAGCAAGGGCTGCTTTTCCACTGTGGGTACCTGGTGATCAG	14565
2373	Qy	GGCAGACTGTGAGGGCCACGGGTTGGGCTGTAGATCTGGGCTGACATCTAGAAATCACTTGC	2432
14566	Db	GGCAGACTGTGAGGGCCACGGGTTGGGCTGTAGATCTGGGCTGACATCTAGAAATCACTTGC	14625
2433	Qy	CACCTGGAGCCTCAGTAAATACCTGGGTGCCCTCTGCTCTCAATCTCCAGAGCCATG	2492
14626	Db	CACCTGGAGCCTCAGTAAATACCTGGGTGCCCTCTGCTCTCAATCTCCAGAGCCATG	14685
2493	Qy	TCCATGGGAGGTGGGCTCTGAAGGGCGAAGTGGGAGGAGGAGGCCCTCTAGGCCTGGG	2552


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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/508,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9695
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002472.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 47
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 17
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 59
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 25
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 22
; US-09-864-761-9695

Query Match          14.0%; Score 377; DB 9; Length 577;
Best Local Similarity 100.0%; Pred. No. 1.4e-94;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2275 GGAATTCCTCTTGGTCCCGGGGGGGCGGGAATTCCTAAGTGTCCACCCCGAGGAGG 2334
Db 577 GGAATTCCTCTTGGTCCCGGGGGGGCGGGAATTCCTAAGTGTCCACCCCGAGGAGG 518

Qy 2335 CAAGGGGCTGTTTCCACTGTGGTACCTGTGATCAGGGCAAGCTGTGGAGGCCAGGG 2394
Db 517 CAAGGGGCTGTTTCCACTGTGGTACCTGTGATCAGGGCAAGCTGTGGAGGCCAGGG 458

Qy 2395 GTGGGGCTGAGACTGGGTGACATCTAGAATCACCCTGCACCTGAGGCTCAGTAAATG 2454
Db 457 GTGGGGCTGAGACTGGGTGACATCTAGAATCACCCTGCACCTGAGGCTCAGTAAATG 398

Qy 2455 CTTGGGTCCTCTGCTCTCAATCTCCAGGCCATGCTCCATGGGAGGTGGGCTCTGA 2514
Db 397 CTTGGGTCCTCTGCTCTCAATCTCCAGGCCATGCTCCATGGGAGGTGGGCTCTGA 338

Qy 2515 AGGGCGAAGGTGGGAGAGCAGGGCCCTTGAAGCCCTGGGTATCCAGAGGGGCCACGTGCA 2574
Db 337 AGGGCGAAGGTGGGAGAGCAGGGCCCTTGAAGCCCTGGGTATCCAGAGGGGCCACGTGCA 278

Qy 2575 CTTGATTCCTCTGGGGCCAGAGAACTGATGTATGTGTGACAAAGTCAACGAGTA 2634
Db 277 CTTGATTCCTCTGGGGCCAGAGAACTGATGTATGTGTGACAAAGTCAACGAGTA 218
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Qy 2635 AGCCAGCAAAAGCCACC 2651
Db 217 AAGCCAGCAAAAGCCACC 201

RESULT 5
US-10-172-118-786
; Sequence 786, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 786
; LENGTH: 1978
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 002561
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-786
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Query Match          9.0%; Score 243.6; DB 15; Length 1978;
Best Local Similarity 58.3%; Pred. No. 3.9e-57;
Matches 501; Conservative 0; Mismatches 329; Indels 30; Gaps 3;

Qy 98 TGGGCTCTCTCGCCCAAAAAGGCTACAGGAGCGGGACCTGGAACCCAGTTTTCATC 157
Db 175 TGGGCTCTCTGATAAAGAGGGTTTACCAAGACGTCGACACCTCCCTGAGAGTGTGTC 234

Qy 158 ATCAACAAACTCAAAGGGTTTCCGTCATCTAGATCAAGAGGCTTGGAAACCGGCTGTG 217
Db 235 ATCAACAAAGTCAAAGGGCGTGGCTTTCACCAACACCTCGGATCTTGGGAGGGATCTGG 294

Qy 218 GATGTGCGGACTCTGTAAGCCACCTCAGGAGGAGAACTGTCTTCTTGTGACCAAC 277
Db 295 GATGTGCGGACTACGTCTATTCAGCCCGAGGAGAACTGTCTTCTTGTGACCAAC 354

Qy 278 TTCTTTGTACGCGCCCAAGTTTCAAGGCGAGATGCCAGAGCACCCGTCCTCCCACTG 337
Db 355 CTGATTGTGACCCCAACCCAGCGGCAAGACGCTGTGCTGAGAACTGAAGGCATTCCTGAT 414

Qy 338 GCTAACTGTGGTCCAGGAGTCTCCCGGAGGGAGGGAGGCACACAGCCAGGT 397
Db 415 GCGCGTGTCTCAAGACAGCGACTCCACGCTGGGGAAGCGTTACAGCTGGAACCGGA 474

Qy 398 GTAAAAACAGGCGCAGTGTGTGGTG---TTCAATGGGACCCACAGGACCTGTGAGATCTGG 454
Db 475 GTGAAGACGGCGCTGCTTGGGAGAGGAACTTGGCCAGGGGCACTGTGAGATCTTT 534

Qy 455 AGTTGTGCGCCAGTGAGAGTGGCGTTGTGCCCTGAGGCCCTGTGTCGCCAGGCCAG 514
Db 535 GCCTGTGCGCCGTGGAGACAAGCTCCAGGCGGGAGGAGCCATTCCTGAAGGAGGCCGAA 594

Qy 515 AACTTCACACTGTTTCATCAAAAACACAGTCACCTTCAGCAAGTTCACTTCTTAAGTCC 574
Db 595 GATTCACCATTTTTCATTAAGAACACACATCCGTTTCCCAAATTCACCTTTCACAAAC 654

Qy 575 AATGCTCTGGAGACCTTGGGACCCCACTATTTAAGCACTGGCGCTATGAACCAACAATTC 634
Db 575 AATGCTCTGGAGACCTTGGGACCCCACTATTTAAGCACTGGCGCTATGAACCAACAATTC 634
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Db 655 AATGTGATGGAGTCAAGGACAGATCTTTCTCCTGAAATCATGCCACTTTTGGCCCCAAG--- 711
 QY 635 AGCCCTTACTGTCGGTGTTCGGCATTTGGGACCTCGTGGCCAAAGCTGTGGAGGACCTTC 694
 Db 712 AACCACTACTCCCCATCTTCGACTGGGCTCCATCGCTGGGCGGGAGCGACTTC 771
 QY 695 GAGGACCTGGGCTGTCTGGGTGGCTCTGTAGGCACTCAGAGTTCACTGGGATTTGACCTG 754
 Db 772 CAGGATATAGCCCTCGAGGTGGCTGATAGAAATTAATTTGAATGAATGTGATCTT 831
 QY 755 GACACCGGGGACTCTGGCTGTGGCTCCTCACTACTCTCTTCAGCTGCGAGGAGAGA----- 809
 Db 832 GATAAAGTGCCTCTGAGTGGACCCCTCACTATTTCTTTAGCCCTCGGCAATAAACTT 891
 QY 810 -----GCTACAACCTTCAGGACAGCCACTCACTGGTGGGAGCAACG 850
 Db 892 TCAAGTCTGTCTCTCCGGGTACACTTCAGATTGCCAGATATTACCAGAGCGAGCC 951
 QY 851 GGTGTGGAGGCCCGACCTCTCAAGCTCTATGGAATTCGGCTTCGACATCTCTGTCACC 910
 Db 952 GGGGTGGAGTTCGGACACCTGATGAAGCCCTACGGGATCCGCTTGACGTGATGGTGAAC 1011
 QY 911 GGGCAGGCGAGGAGTTCGG 930
 Db 1012 GGCAAGGTGCTTTCTTCTG 1031

RESULT 6

; Sequence 786, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van de Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 786
 ; LENGTH: 1978
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-786

Query Match 9.0%; Score 243.6; DB 16; Length 1978;
 Best Local Similarity 58.3%; Pred. No. 3.9e-57;
 Matches 501; Conservative 0; Mismatches 329; Indels 30; Gaps 3;
 QY 98 TGGGCTCTCTCCGCAAAAAGGTACAGAGCGGACCTGGAAACCCCAAGTTTTCATC 157
 Db 175 TGGGTGTTCTGATAAAGAGGGTTACCAAGCTCGACACCTCCCTGCGAGGTGCTGC 234
 QY 158 ATCAACAACTCAAGGGTTTCGTCATCAAGAGCTTGGAAACCGGCTGTGG 217
 Db 235 ATCAACAAAGTCAAGGGCGTGGCCCTTCAACCAACCTCGGATCTTGGCGAGCGGATCTGG 294
 QY 218 GATGTGGCCGACTTCGTGGAACCCACCTCAGGAGAGAACGTGTCTTCTTGGGTGACCAAC 277
 Db 295 GATGTCCCGGCTAGTCAITTCAGCCAGGAGAGAACGTCTTTTGTGGTCAACCAAC 354

QY 278 TTCTTGTGACCCAGCCCAAGTTTCAGGCGAGATGCCAGAGCACCCCTCGTCCCTCCACTG 337
 Db 355 CTGATTGTGACCCCAACCCAGCGGAGAACGTCGTGCTGAGATGAAGGCAATCTCTGAT 414
 QY 338 GCTAATCTGTGGTTCGAGAGACTGCCCCGAAAGGGAGGAGGACACACAGCCACGGT 397
 Db 415 GCGCGGTGCTCCAGGACAGCGACTGCCAGCTGGGGAAGCGGTTACAGCTTGGAAACGGA 474
 QY 398 GTAAAAACAGGCCAGCTGTGTGTG---TTCAATGGGACCCACAGGACCTGTGAGATCTGG 454
 Db 475 GTGAGACCGGCGCTGCTCGGAGAGGGAACTTGGCCAGGGCACCTGTGAGATCTTT 534
 QY 455 AGTGTGGTCCCAAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGCCCCAGGCCAG 514
 Db 535 GCGTGTGCTCCGTTGGAGACAAGCTCCAGGCGGAGGAGCCATTCCTGAAGAGGCGCGAA 594
 QY 515 AACTTCACACTGTTTCATCAAAACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTCC 574
 Db 595 GACTTCACCAATTTTATAAAGAACCAATCCGTTTCCCAATTCACCTTCTCCAAAC 654
 QY 575 AATGCTTTGGAGACCTGGGACCCACCTATTTTAAAGCACTCCGCTATGAACCAAAATTC 634
 Db 655 AATGTGATGGAGCTCAAGGACAGATCTTTCTGAAATCATGCCACTTTTGGCCCAAG--- 711
 QY 635 AGCCCTTACTGTCGGTGTTCGGCATTTGGGACCTCGTGGCCAAAGCTGTGGAGGACCTTC 694
 Db 712 AACCACTACTGCCCATCTTCGACTGGGCTCCATCTGTCGCTGGGCGGAGGAGCACTTC 771
 QY 695 GAGGACCTGGGCTGCTGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATTTGACCTG 754
 Db 772 CAGGATATAGCCCTCGAGGTGGCTGATAGGAATTAATTTGAATGAAGTGTGATCTT 831
 QY 755 GACACCGGGGACTCTGGTGTGCTGGCTCACTACTCTCTTCAGCTGCGAGGAGAGA----- 809
 Db 832 GATAAAGTGCCTCTGAGTGGCACCCCTCACTATTTCTTTAGCCGCTGTGCAATAAACTT 891
 QY 810 -----GCTACAACCTTCAGGACAGCCACTCACTGGTGGGAGCAACG 850
 Db 892 TCAAGTCTGTCTCTCCGGGTACAACTTCAGATTGCCAGATATTACCAGAGCGAGCC 951
 QY 851 GGTGTGGAGGCCCGACCCCTCTCAAGCTCTATGGAATTCGGCTTCGACATCTCTGTCACC 910
 Db 952 GGGGTGGAGTTCGGACACCTGATGAAGCCCTACGGGATCCGCTTGACGTGATGGTGAAC 1011
 QY 911 GGCAGGCGAGGAGTTCGG 930
 Db 1012 GGCAAGGTGCTTTCTTCTG 1031

RESULT 7

US-09-833-082-1
 ; Sequence 1, Application US/09833082
 ; Patent No. US20020151480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chun, Miyoung
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 10218
 ; FILE REFERENCE: MNI-227
 ; CURRENT APPLICATION NUMBER: US/09/833,082
 ; CURRENT FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1389
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-09-833-082-1

Query Match 8.9%; Score 239.2; DB 9; Length 1389;
 Best Local Similarity 56.3%; Pred. No. 5.7e-56;
 Matches 529; Conservative 0; Mismatches 378; Indels 33; Gaps 3;
 QY 152 TCATCATCAACCAACTCAAGGGGTTTCCCTCACTCAGATCAAGGAGCTTGGAAACCGG 211

Db 214 TCCGTTACGACCAAGGTCAAGGGCGTGTGTGACCAACACTTTAAACTTGGATTCGG 273
Qy 212 CTGTGGGATGTGGCCCACTTCGTGAAGCCACTCAGGAGAGAACTGTTCTTCTTGTG 271
Db 274 ATCTGGGATGTGGCGGATATGTGATACAGCTCAGGAGGAATCTCCTCTTGTGATG 333
Qy 272 ACCAACTCTTGTGACCGCAGCCCAAGTTTCAAGGAGATGCCAGAGACCCGTCGTC 331
Db 334 ACCAACTGATCTCACCATCAACAGACACAGGCGCTGTGCCCGAGATTC---CAGAT 390
Qy 332 CCACCTGGTAACTGTGGTGTGACAGGACTGCCCGAAGGGAGGAGGACACACAGC 391
Db 391 GGGACCATGTGTGTAATCATGATGCCAGCTGTACTGCCGCTGTGCCGACCCACAGC 450
Qy 392 CACGCTGTAAACAGGCGAGTGTGTGTTCAATGGACCCACAGACCTGTGAGATC 451
Db 451 AACGAGTCTCAACAGGAGGTGCTAGCTTTCAACGGGTCCGTCAAGACGTGTGAGTG 510
Qy 452 TGGAGTTGGTCCAGTGGAGAGTGC---GTTGTGCCCTCGAGGCCCTCTGCCCGAG 508
Db 511 GCGGCTGTGTCGCGGTGGAGATGACACACAGTGCACACCTGCTTTTAAAGGCT 570
Qy 509 GCCAGAACTTCACTGTTTCAATAAACACAGTCACTTTCAGCAAGTTCAACTTCTCT 568
Db 571 GCAGAAACTTCACTCTTTTGGTTAAGAAACACATCTGTATCCCAATTTAATTCAGC 630
Qy 569 AAGTCCATGCTTGGACACTGGACCCCACTTATTTAAGACTGCGGCTATGAACCA 628
Db 631 AAGAGGAATATCTTCCCAACATCACCACTACTTACCTCAAGTGTGANTATGATGCT 690
Qy 629 CAATTCAGCCCTACTGTCCGCTGTTCCGATTTGGGACCTCGTGGCCAGAGCTGGAGG 688
Db 691 AAACAGATCCCTTCTGCCCATATTCGTTTGGCAAAATAGTGGAGACGAGGACAC 750
Qy 689 ACCTTCAGGACCTGTGGCTGTGGTGTGTTAGGCATCAGAGTTCACTGGGATGT 748
Db 751 AGTTTCCAGGACATGGCCGTGGAGGAGGCATCATGGGCATCCAGGTCAACTGGGACTGC 810
Qy 749 GACCTGGACACCGGGACTCTGGCTGTGGCTCACTACTCTTCCAGCTGCAGGAGA-- 806
Db 811 AACCTGGACAGCGCCCTCCCTTCTGTTCGCCAGGTACTCTCTTCGCCGCTCGATACA 870
Qy 807 -----AGAGCTACAACTTTCAGGACAGCCACTCACTGTGTG 841
Db 871 CGGACGTTGAGCACACAGTATCTCTCGCTGACAAATTCAGTTTGGCAAGTACTACAGA 930
Qy 842 GAGCAACCGGTGTGGAGCCCGACACCTGCTCAAGCTCTATGGAATCCGCTTCGACATC 901
Db 931 GACCTGGTGGCAACGACGACGACGCTCATCAAGGCTTATGGCATCCGCTTCGACATC 990
Qy 902 CTGCTCACGGGACGAGGGAAGTTCCGGCTCATCCCGCCGCTCACACTGGGACCC 961
Db 991 ATTGTTTGGAGGACGAGGAATTTGACATCATCCCATATGATCAACATCGGCTCT 1050
Qy 962 GGGGAGCTGTGGCGGTGGTCACTTTTGTGACCTGTCTACTGTCTGTATGTGAT 1021
Db 1051 GGCCTGGCACTGTAGGATGGCAGCCGCTGTGTGTGACATCATAGTCTCTACTGCAATG 1110
Qy 1022 AGAGAGCCCATTTCTACTGGAGGACAAAGTATGAGGAG 1061
Db 1111 AAGAAAGACTTACTATTCGGGAGAGAAATATAAATATG 1150

RESULT 8
US-10-305-720-831
; Sequence 831, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720

; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO: 831
; LENGTH: 1750
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inceyte ID No. US20040010136A1 555697
US-10-305-720-831

Query Match 8.9%; Score 239.2; DB 16; Length 1750;
Best Local Similarity 56.3%; Pred. No. 6.2e-56;
Matches 529; Conservative 0; Mismatches 378; Indels 33; Gaps 3;

Qy 152 TCCATCATCAACAACTCAAGGGGTTTCCGTCACCTCAGATCAAGAGGCTTGGAAACCG 211
Db 214 TCCGTTACGACCAAGGTCAAGGCGTGTGTGACCAACACTTCTTAACTTGGATTCGG 273
Qy 212 CTGTGGATGTGGCCGACTTCGTGAAGCCACTCAGGAGAGAACTGTTCTTCTTGGTG 271
Db 274 ATCTGGATGTGGCGGATATGTGATACAGCTCAGGAGGAAACTCCCTCTTGTGATG 333
Qy 272 ACCAACTTCTTGTGACCGCAGCCCAAGTTTCAAGGAGATGCCAGAGACCCGTCGTC 331
Db 334 ACCAACTGATCTCTACCATGAACACAGACAGGCGCTGTGCCCGAGATTC---CAGAT 390
Qy 332 CCACCTGGCTAACTGTCTGGGTTCAGGAGACTGCCCGAAGGGAGGAGGACACACAGC 391
Db 391 GCGACCACTGTGTGTAATCAGATGCCAGCTGTACTGCCGCTCTGCCGACCCACAGC 450
Qy 392 CACGCTGTAAACAGGCGAGTGTGTGTTCAATGGACCCACAGGACCTGTGAGATC 451
Db 451 AACGAGTCTCAACAGGAGGTGCGTAGCTTTTCAACGGGTCCGTCAAGACGTGTGAGTG 510
Qy 452 TGGAGTTGTGGCCAGTGGAGAGTGC---GTTGTGCCCTCGAGGCGCTCTTCTTAAAGGCT 570
Db 511 GCGGCTGTGTCGCGGTGGAGATGACACAGTGCACACCTGCTTTTAAAGGCT 570
Qy 509 GCCAGAACTTCACTGTTTCAATAAACACAGTCACTTTCAGCAAGTTCAACTTCTCT 568
Db 571 GCAGAAACTTCACTCTTTTGGTTAAGAAACACATCTGTGATCCCAAAATTTAATTCAGC 630
Qy 569 AAGTCAATGCTTGGAGACTGGGACCCCACTATTTAAGCACTGCCGCTATGAACCA 628
Db 631 AAGAGAAATATCTTCCCAACATCACCACTACTTACCTCAAGTGTGCAATTTATGATCT 690
Qy 629 CAATTCAGCCCTACTGTCTCCGCTTTCGCAATTTGGGACCTCGTGGCCAGGCTGGAGG 688
Db 691 AAACAGATCCCTTCTGCCCATATTCGTTTGGCAAAATAGTGGAGAACGAGGACAC 750
Qy 689 ACCTTCAGGACCTGTGGCTGTGGTGTGTTAGGCATCAGAGTTCACTGGGATGT 748
Db 751 AGTTTCCAGGACATGGCCGTGGAGGAGGCATCATGGGCATCCAGGTCAACTGGGACTGC 810
Qy 749 GACCTGGACACCGGGACTCTGGCTGTGGCTCACTACTCTTCCAGCTGCAGGAGA-- 806
Db 811 AACCTGGACAGCGCCCTCCCTCTGTTCGCCAGGTACTCTCTTCGCCGCTCGATACA 870
Qy 807 -----AGAGCTACAACTTTCAGGACAGCCACTCACTGTGTG 841
Db 871 CGGACGTTTACGACCAACAGTATCTCTCGCTGACAAATTCAGTTTGGCAAGTACTACAGA 930
Qy 842 GAGCAACCGGTGTGGAGCCCGACACCTGCTCAAGCTCTATGGAATCCGCTTCGACATC 901
Db 931 GACCTGGTGGCAACGAGCAGCGACGCTCATCAAGGCTTATGGCATCCGCTTCGACATC 990
Qy 902 CTGCTCACGGGACGAGGGAAGTTCCGGCTCATCCCGCCGCTCACACTGGGACCC 961
Db 991 ATTGTTTGGAGGACGAGGAATTTGACATCATCCCATATGATCAACATCGGCTCT 1050
Qy 962 GGGGAGCTGTGGCGGTGGTCACTTTTGTGACCTGTCTACTGTCTGTATGTGAT 1021
Db 1051 GGCCTGGCACTGTAGGATGGCAGCCGCTGTGTGTGACATCATAGTCTCTACTGCAATG 1110
Qy 1022 AGAGAGCCCATTTCTACTGGAGGACAAAGTATGAGGAG 1061
Db 1111 AAGAAAGACTTACTATTCGGGAGAGAAATATAAATATG 1150

QY 962 GGGGCGAGTGGCTGGTCAACCTTTTCTGTGACCTGCTACTGCTGTATGTGGAT 1021
Db 1051 GGCCTGGCACTGCTAGGATGGGACCGTGTGTGTGACATCATAGTCTCTACTGCGATG 1110
QY 1022 AGAGAAGCCCAATTTCTACTGAGGACAAAGTATGAGGAGG 1061
Db 1111 AAGAAAGACTCTACTATCGGAGAGAAATATAATATG 1150

RESULT 9

US-10-128-558-20
; Sequence 20, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 20
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
US-10-128-558-20

Query Match 8.8%; Score 237.6; DB 18; Length 1269;

Best Local Similarity 56.2%; Pred. No. 1.5e-55;
Matches 528; Conservative 0; Mismatches 379; Indels 33; Gaps 3;

QY 152 TCCATCATACCAAACTCAAGGGTTTCGGTCACTCAGATCAAGGAGCTTGGAAACCGG 211
Db 187 TCCGTTACGACCAAGGCTCAAGGGCTGCTGTGACCAACACTTCTAAACTTGGATCCGG 246
QY 212 CTGTGGGATGTGGCGGACTTGTGAAGCCACCTCAGGAGAGACGTGTTCTTCTTGGTG 271
Db 247 ATCTGGGATGTGGCGGATATGTGATACAGCTCAGGAGAAACTCCCTCTTCGTCATG 306
QY 272 ACCAACTTCTTGTGACGCCAGCCAAAGTTTCAGGGCAGATGCCCGAGACACCGCTCCGTC 331
Db 307 ACCAAGCTGATCCCTCACCATGACCAACAGACACAGGGCTGTGCCCCGAGATTC---CAGAT 363

QY 332 CCACCTGGCTAACTGCTGGGTGCGAGGACTGCCCGAAGGGGAGGAGGCACACACAGC 391
Db 364 GCGACCACTGTGTGTAATAATCAGATGCCAGCTGTACTGCCGGCTCTGCCGGCACCCACAGC 423
QY 392 CACGGTGTAAACACAGGCGAGTGTGTGTGTCAATGGAGCCACAGACAGCTGTGAGATC 451
Db 424 AACGGAGTCTCAACAGGAGGTCGTACTTTCAACGGGTCTGTCAAGACGTGTGAGGTG 483
QY 452 TGGAGTGTGTGCCCGCAGTGGAGAGTGGC---GTTGTGCCCTCGAGGCCCTCTCTGGCCAG 508
Db 484 GCGGCTGTGTGCCCGTGGAGATGACACACAGCTGCCACAACCTGCTTTTAAAGGCT 543
QY 509 GCCCAGAACTTCACACTGTTTCATCAAAAACAGCTCACTTCAGCAAGTTCACACTTCTCT 568
Db 544 GCAGAAAACTTCACCTCTTTTGGTTAAGAACACATCTGGTATGCCAAATTTAAATTCAGC 603
QY 569 AAGTCCAAATGCTTGGAGACCTGGGACCCCACTATTTTAAAGCACTGCGGCTATGAACCA 628
Db 604 AAGAGGAATATCTTCCCAACATCACCACTACTTACCTCAAGTCGTGATTTATGATGCT 663
QY 629 CAATTCAAGCCCTACTGTCCCGTGTTCGCAATTTGGGACCTCTGTGGCCCAAGCTGGAGG 688
Db 664 AAAACAGATCCCTTCTGCCCATATTCGCTTGGCAAAATAGTGGAGACGCGAGGACAC 723
QY 689 ACCTTCGAGGACCTGGCGTGTGTGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATGT 748
Db 724 AGTTTCCAGGACATGGCGTGGAGGAGGATCATGGSCATCCAGGTCACTTGGAGCTGC 783
QY 749 GACCTGGACACCGGGGACTCTGGCTGTGGCTCACTACTCTCTTCCAGCTCCAGGAGA-- 806
Db 784 AACCTGGACAGAGCGCTCTCTGTCTGTGCCAGGTACTCTTCCGGCGCTCGATACA 843
QY 807 -----AGAGCTACAACCTTCAGGACAGCACTCACTGGTGG 841
Db 844 CGGAGCTGTGACACAACAGTATCTCTGGCTACAAATTCAGGTTGCCAAGTACTACAGA 903
QY 842 GAGCAACCGGGTGTGGAGCGCCGACCCCTGCTCAAGCTCTATGGAATCCGCTTCGACATC 901
Db 904 GACCTGGCTGGCAGCAGCAGCGCTCATCAAGGCTATGGCACTCCGCTTCGACATC 963
QY 902 CTCGTACCGGCGAGGAGGAAAGTTCGGGTCTATCCCGCGGCGTCACACTGGGACCC 961
Db 964 ATTGTGTTTGGAGGAGGAGGAAATTTGACATCATCCCACTATGATCAACATCGGCTCT 1023
QY 962 GGGGCGAGTGTGCTGGGCGTGTCACTCTTTTGTGACCTGCTACTCTGTATGTGGAT 1021
Db 1024 GGCCTGGCACTGCTAGGATGGCGACCTGCTGTGTGACATCATAGTCTCTACTGTCATG 1083
QY 1022 AGAGAAGCCCAATTTCTACTGAGGACAAAGTATGAGGAGG 1061
Db 1084 AAGAAAGACTCTACTATCGGAGAGAAATATAATATG 1123

RESULT 10

US-10-386-414-18
; Sequence 18, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: 55092 AND 10218 MOLECULES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282

; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-386-414-18

Query Match
Best Local Similarity 8.8%; Score 237.2; DB 16; Length 1167;
Matches 527; Conservative 1; Mismatches 379; Indels 33; Gaps 3;

QY 152 TCATCATCAACAACTCAAGGGTTCCTGCTCAGATCAAGAGCTTGGAAACGG 211
DB 187 TCCGTTACGACCAAGTCAAGGGCTGTGTGACCAACACTTCAAACTTTGGATTCCGG 246
QY 212 CTGTGGGATGGCGACTTCGTGAAGCCACTCAGGAGAGAAAGTTCCTTCTGTG 271
DB 247 ATCTGGGATGGCGGATATGTATACCATGCTCAGGAGGAAATCCCTCTTGTGATG 306
QY 272 ACCAACTTCCTTGTGACGCCACCCCAAGTTCAGGGCAGATGCCAGAGCACCCTGCTC 331
DB 307 ACCAAGGTGATCTCCACATGAACACAGACAGAGGCTGTGCCCGAGATTC--CAGAT 363
QY 332 CCATCGGCTTAAGTGTGGGTGACAGAGACTGCCCCAGGGAGGAGGACACACAGC 391
DB 364 GCGACCACTGTGTGTAATATCAGATCCAGCTGTACTGCGGGCTCTGCGGACCCACAGC 423
QY 392 CACGTGTAAACAAAGCCAGTGTGTGTGTTCAATGGACCCACAGGACCTGTGAGATC 451
DB 424 AACGAGTCTCAACAGGAGGTGCGTAGCTTCAACGGGTCTGTCAAGACGTGTGARGTG 483
QY 452 TGGAGTTGGTCCCAAGTGAGAGTGGC---GTGTGCCCCCTCAGGCCCTCTGCCCCAG 508
DB 484 GCGGCTGTGTGCGGTGGAGATGACACACAGCTGCCACACCTGCTTTTAAAGGCT 543
QY 509 GCCAGAACTTCACACTGTTCAATCAACAAACACAGTCACTTCAGCAAGTTCACCTCTCT 568
DB 544 GAGAAACTTCACCTCTTTGGTTAAGAACACATCTGATATCCAAATTTAATTTACG 603
QY 569 AAGTCCAATGCTTGGAGACCTGGGACCCCACTATTTTAAAGCACTGCGGCTATCAACCA 628
DB 604 AAGAGGAATATCTTCCCAACATACCACTACTTACCTCAAGTCGTGATTTATGCT 663
QY 629 CAATTACGCCCTACTGTCCCGTGTTCGCAATGGGGACCTCGTGGCCCAAGCTGGAGGG 688
DB 664 AAACAGATCCCTTCTGCCCATATATTCGCTCTTGGCAAAATAGTGGAGACGACGAC 723
QY 689 ACCTTCGAGGACTGGCGTGTGTGGTGTCTGTAGGCATCAGAGTTCATCTGGGATGT 748
DB 724 AGTTCCAGGACATGGCGGTGAGAGGAGGCATCATGGGCATCCAGTCACTGGGACTGC 783
QY 749 GACCTGGACACGGGAGACTGTGGCTGTGCTGCTACTACTCTTCCAGCTCAGAGAGA-- 806

DB 784 AACCTGGACAGAGCGGCTCCCTCTGCTGCTCCAGGTAATCTCTTCCGCGCCTCGATACA 843
QY 807 -----AGAGTCAAACTTACGACAGCAGCCTCACTCTGTGG 841
DB 844 CGGAGCGTTGAGCACACAGTATCTCTGCTGCTACAAATTCAGGTTTGCCAAAGTACTACAGA 903
QY 842 GAGCAACCGGGTGTGGAGGCCGACCCCTGCTCAAGCTCTATGAATCCGCTTTCGACATC 901
DB 904 GACCTGGCTGCAACGAGCAGCAGCTCATCAAGCCCTATGGCATCCGCTTCGACATC 963
QY 902 CTCGTACCGGCGGAGGAGGAGTTTGGGCTCATCCCCAGCGGCTTCACACTGGGACCC 961
DB 964 ATTGTGTTGGGAAGCGAGGAAATTTGACATCATCCCCACTATGATCAACATCGGCTCT 1023
QY 962 GGGCAGCTTGGCTGGCGTGTGCTACCTTTTCTGTGACCTGCTGCTGATGTGGAT 1021
DB 1024 GGCTGCACTGTAGCATGGGACCGTCTGTGACATCATAGTCTCTTACTGATG 1083
QY 1022 AGAGAAGCCCATTTCTACTCGGAGCAAAAGTATGAGGAGG 1061
DB 1084 AAGAAAGACTCTACTATCGGAGAGAAATATAATATG 1123

RESULT 11
US-10-386-414-16
; Sequence 16, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: MPI03-0210MIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-386-414-16

Query Match
Best Local Similarity 8.8%; Score 237.2; DB 16; Length 2048;
Matches 527; Conservative 1; Mismatches 379; Indels 33; Gaps 3;

Db 1153 CGGAGCTTTGACACAAAGTATCTCTCTGGCTACAATTTACAGTTTGGCAAGTACTACAGA 1212
QY 842 GAGCAACCGGGTGTGAGGCGCCGACCTCTCTCAAGCTCTATGGAATCGGTTTCGACATC 901
Db 1213 GACCTGGCTGGCAACGAGCAGCGCAGCTCATCAAGGCTATGGCATCGCTTCGACATC 1272
QY 902 CTCCTCACCGGCGAGCGAGGGAAGTTCGGGCTCATCCCCACGCGCTCACACTGGGCACC 961
Db 1273 ATTGTGTTTGGGAAGCGAGGGAATTTGACATCATCCCCACTATGATCAACATCGGCTCT 1332
QY 962 GGGGCGAGCTTGCTGGCGCTGTGCTACCTTTTCTGTGACCTGCTACTGCTGTATGTGGAT 1021
Db 1333 GGCCTGGCACTGCTAGGCGATGCGACCGTGTGTGTGACATCATAGTCTCTACTGCAATG 1392
QY 1022 AGAGAAGCCCATTTCTACTGAGGAGCAAAAGTATGAGGAGG 1061
Db 1393 AAGAAAAGACTCTACTATCGGAGAGAAATATAAATATG 1432

RESULT 13

US-10-187-659A-4
; Sequence 4, Application US/10187659A
; Publication No. US20040002152A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF P2X4 EXPRESSION
; FILE REFERENCE: RTS-0379
; CURRENT APPLICATION NUMBER: US/10/187,659A
; CURRENT FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 4
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (310) ... (1476)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 789
; OTHER INFORMATION: n = A,T,C or G
US-10-187-659A-4

Query Match 8.8%; Score 236.6; DB 16; Length 2048;
Best Local Similarity 56.1%; Pred. No. 3.5e-55;
Matches 527; Conservative 0; Mismatches 380; Indels 33; Gaps 3;
QY 152 TCCATCATCACCAAACTCAAGGGGTTTCGGTCACTCAGATCAAGGAGCTGGAAACCGG 211
Db 496 TCCGTTACGCAAGGTCAAGGGGCTGGCTGTGACCAACACTTCTAAACITTTGGATTCGG 555
QY 212 CTGTGGGATGTGGCGCACTTCGTGAAGCCACTCAGGAGAGAACGTGTTCTTCTTGTG 271
Db 556 ATCTGGGATGTGGCGGATTTGTGATACAGCTCAGGAGAACTCCCTCTTGTGTCATG 615
QY 272 ACCAATCTCTTGTGAGCCGACCCCAAGTTTCAAGGCGAGATCCCAAGACACCCCTCCGTC 331
Db 616 ACCAAGCTGATCCTCACCATGAACACAGACAGGGGCTGTGCCCGAGATTCTCAGAT 672
QY 332 CCACCTGGCTACTGTGGTTCGACGAGCTGCCCGGAGGGGAGGAGGACACACAGC 391
Db 673 GGGACACTGTGTAAATCAGATGCCAGCTGTACTGCCGGCTTTCGCGGACCCACAGC 732
QY 392 CACGGTGTAAAAACAGGCGAGTGTGTGTTTCAATGGGACCCACAGACCTGTGAGATC 451
Db 733 AACGGAGTCTCAACAGGCGAGTGTGTGTTTCAACGGGTCTGTCAAGACGTGTGANGTG 792
QY 452 TGGAGTTGTGTCAGTGTGAGAGTGGC---GTTGTGCCCTCAGGCCCTCTGTCGCCAG 508
Db 793 GCGGCTGTGTGCCGGTGGAGATACACACAGCTGTGCCACCACTGTCTTTTAAAGGCT 852
QY 509 GCCCAGAACTTCACACTGTTCATCAAAAACACAGTCACCTTCAGCAAGTTCAACTTCTCT 568

Db 853 GCAGAAAACITTCATCTTTTGGTTAAGAACAAACATCTGGTATCCCCAAATTTAATTTACG 912
QY 569 AAGTCCCAATGCCCTGGAGACCTGGGACCCCACTATTTTAAAGCACTGCCGCTATGAACCA 628
Db 913 AAGAGGAATATCTTCCCAACATCACCACCTACTTACCTCAAGTCGTGCAATTTATGATGCT 972
QY 629 CAATTCAAGCCCTACTGTCCTCCGTTTCCGCAATTTGGGACCTCTGTGGCCAAAGGCTGAGGG 688
Db 973 AAAACAGATCCCTTCTGCCCAATATTCCTGTTTGGCAAAATAGTGAGAAACGAGGACAC 1032
QY 689 ACCTTCAGGACCTGGGCTTGTGGGTGCTGTAGGCATCAGAGTTCACTGGGATTTGT 748
Db 1033 AGTTTCCAGACATGCGCTGGAGGAGGATCATGGGCATCCAGTCACTGGGACTGC 1092
QY 749 GACCTGACACCGGGGACTCTGGCTGCTGGCTCTACTTCTTCAGCTGTCAGGAGA-- 806
Db 1093 AAGCTGGACAGACGCGCTCCCTCTGCTGCCAGGTACTCTCTTCCGCGCTCGATACA 1152
QY 807 -----AGAGTACAATTCAGGACACGCCACTCACTGCTGG 841
Db 1153 CGGACGTTGAGCACAAAGTATCTCTGGCTACAATTTAGGTTTGCCAAAGTACTACAGA 1212
QY 842 GAGCAACCGGGTGTGAGGCGCCGCACTCTCAAGCTCTATGGAATCCGCTTTCGACATC 901
Db 1213 GACCTGCTGCAACGAGCAGCGCTCATCAAGSCCTATGCACTCGCTTCGACATC 1272
QY 902 CTGCTACCGGCGAGGAGGAAAGTTGGGCTCATCCCAAGCCGCTCACTGGGACCC 961
Db 1273 ATTGTGTTTGGGAAAGCAGGGAATTTGACATCATCCCCACTATGATCAACATCGGCTCT 1332
QY 962 GGGGCGAGTTGGCTGGGCGGTGTCACCTTTTCTGTGACCTGCTACTGCTGTATGTGGAT 1021
Db 1333 GGCCTGGCACTGTAGGATGGCGCGTGTGTGACATCATAGTCTCTACTGCAATG 1392
QY 1022 AGAGAAGCCCATTTCTACTGAGGACAAAGTATGAGGAGG 1061
Db 1393 AAGAAAAGACTCTACTATCGGAGAGAAATATAAATATG 1432

RESULT 14

US-09-969-347-225
; Sequence 225, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-89
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,598
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,604
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 225
; LENGTH: 2633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-347-225

Query Match 8.7%; Score 233.4; DB 9; Length 2633;
Best Local Similarity 56.7%; Pred. No. 3e-54;
Matches 526; Conservative 0; Mismatches 371; Indels 30; Gaps 4;
QY 164 AAATCAAGGGGTTTCCGTCATCATCAGATCAAGGAGCTTGGAAACCGGCTGTGGGATG 223
Db 398 AAATCAAGGGGCTGGCCGTGACCCAGTCCCTGGCCTCGGCCCCAGGCTCGGATG 457
QY 224 GCGGACTTCGTGAAGCCACTCAGGAGAGAAAGTCTTCTTCTTGTGTGACCACTTCCTT 283
Db 458 GCTGACTACGTCTTCCAGCCCGAGGGGACAACTCTCTCGTGTGTCATGACCAATTCATC 517

Db 849 CTGTCCCGAGTCTCCAGCTTGGCTACGTGGTGCAGAGTCAAGCCAGAACTTCAGCACC 908
QY 701 CTGGCTTGGCTGGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATTGTGACCTGGACACC 760
Db 909 CTGGCTGAGAGGGTGGAGTGGTGGCATCACCATCGACTGGCACTGTGACCTGGACTGG 968
QY 761 GGGGACTCTGGCTGTGGCTCCTACTCTCTCCAGCTTCCAGCTGAGGAGAGA----- 809
Db 969 CACGTACGGCACTGCAGACCCCATCTATGAGTTCCATGGGCTGTACGAGAGAAAAATCTC 1028
QY 810 -----GCTACAACTTCAGACACGCCACTCACTGGTGGGAGCAACCGGGTGTGGAGGCC 862
Db 1029 TCCCAGGCTTCAACTTCAGTTTGGCAGGCACITTTGGAGAC---GGGACCAACTAC 1085
QY 863 CGCACCTGTCTAAGCTCTATGGAAATCCGCTTCGACATCCTCGTCAACCGGCGCAGGCAGGG 922
Db 1086 CGTCACCTCTTCAAGGTGTTGGGATTGGCTTTGACATCCTGGTGGACGGCAAGGCCGGG 1145
QY 923 AAGTTCGGGCTCATCCCGCCGCTCACACTGGGCGGGGCGAGCTTGGCTGGGGTG 982
Db 1146 AAGTTTGACATATCCCTACAAATGACCACTCGGCTCTGAAATTGGCAATCTTTGGGGTG 1205
QY 983 GTCACTTTTCTGTGACCTGCTACTGTGTATGTGGATAGAGAAGCCCATTTCTACTGG 1042
Db 1206 GCCACAGTTCCTGTGACCTGCTGCTGCTTACATCCTGCTCCTAGAGGCCACTACTACAAG 1265
QY 1043 AGGACAAAGTATGAGGAGGCCAAGGCC 1069
Db 1266 CAGAGAAGTTCAATACGCTGAGGAC 1292

Search completed: November 22, 2004, 08:18:16
Job time : 1337.37 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 12:30:45 ; Search time 224.653 Seconds
(without alignments)
8520.488 Million cell updates/sec

Title: US-09-820-095B-1
Perfect score: 2693
Sequence: 1 ttgtctgactatgttgcgcgc.....aaaaaaaaaaaaaaaaaaaaa 2693

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/ECTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1515.4	56.3	1697	3	US-09-381-681-2
2	1162.4	43.2	1360	3	US-09-191-136-30
3	1155.8	42.9	1293	3	US-09-381-681-1
4	394.4	14.6	396	3	US-09-191-136-28
5	239.2	8.9	1750	4	US-09-016-434-831
6	239.2	8.9	1762	2	US-08-742-621-2
7	237.6	8.8	1206	3	US-09-191-608-21
8	233.4	8.7	2643	2	US-08-750-134A-10
9	233.4	8.7	2643	3	US-09-363-745-10
10	233.4	8.7	2643	4	US-09-023-655-897
11	225.4	8.4	1997	2	US-08-750-134A-6
12	225.4	8.4	1997	3	US-09-363-745-6
13	214.4	8.0	1421	3	US-09-191-608-14
14	213.2	7.9	1436	3	US-09-191-608-13
15	206	7.6	1837	2	US-08-750-134A-4
16	206	7.6	1837	3	US-09-363-745-4
17	200.2	7.4	237	3	US-09-191-136-29
18	199.4	7.4	1499	3	US-09-191-608-16
19	168.6	6.3	1243	3	US-09-191-136-15
20	156.2	5.8	1272	3	US-09-191-136-13
21	155.4	5.8	1349	3	US-09-191-608-15
22	155.4	5.8	1753	2	US-08-750-134A-8
23	155.4	5.8	1753	3	US-09-363-745-8
24	131.2	4.9	961	4	US-09-023-655-370
25	103.8	3.9	1853	3	US-08-842-079-19
26	103.8	3.9	1853	4	US-09-638-857-19
27	99.8	3.7	3540	3	US-08-842-079-16

28	99.8	3.7	3540	4	US-09-638-857-16	Sequence 16, Appl
29	94	3.5	94	3	US-09-191-136-18	Sequence 18, Appl
30	92.4	3.4	394	3	US-09-191-136-27	Sequence 27, Appl
31	90.4	3.4	878	1	US-07-915-934-3	Sequence 3, Appl
32	90.4	3.4	878	1	US-08-325-743-3	Sequence 3, Appl
33	83.2	3.1	531	3	US-09-191-608-8	Sequence 8, Appl
34	64.2	2.4	221	3	US-09-191-608-1	Sequence 1, Appl
35	64.2	2.4	910	3	US-09-191-608-2	Sequence 2, Appl
36	56.6	2.1	1872	3	US-09-801-052-1	Sequence 1, Appl
37	56.6	2.1	1872	4	US-10-020-121-1	Sequence 1, Appl
38	55.8	2.1	7218	1	US-08-232-463-14	Sequence 14, Appl
39	54.8	2.0	903	5	PCT-US95-06406A-21	Sequence 21, Appl
40	54.4	2.0	558	4	US-09-043-861-3	Sequence 3, Appl
41	54.2	2.0	183	3	US-09-014-416-60	Sequence 60, Appl
42	54.2	2.0	200	3	US-09-014-416-64	Sequence 64, Appl
43	54.2	2.0	9595	3	US-09-014-416-4	Sequence 4, Appl
44	54.2	2.0	9599	3	US-09-014-416-2	Sequence 2, Appl
45	54.2	2.0	9599	3	US-09-014-416-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-381-681-2
; Sequence 2, Application US/09381681
; Patent No. 6255472
; GENERAL INFORMATION:
; APPLICANT: TAKINO, Takashi
; APPLICANT: NAKAMURA, Yusuke
; TITLE OF INVENTION: HUMAN GENES
; FILE REFERENCE: 055876
; CURRENT APPLICATION NUMBER: US/09/381,681
; CURRENT FILING DATE: 2000-01-10
; EARLIER APPLICATION NUMBER: JPA 9-093044
; EARLIER FILING DATE: 1997-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(1338)
US-09-381-681-2

Query Match	56.3%	Score 1515.4	DB 3	Length 1697
Best Local Similarity	99.6%	Pred. No. 0		
Matches 1512	Conservative	0	Mismatches 6	Indels 0
				Gaps 0
QY	97	GTGGGCTCTCTCGCCAAAAAGGCTACAGAGCGGGACCTGGAAACCCAGTTTCCAT	156	
Db	180	GTGGGCTCTCTCGCCAAAAAGGCTACAGAGCGGGACCTGGAAACCCAGTTTCCAT	239	
QY	157	CATCAACAACTCAAAAGGGTTTCCGTCACTCAGATCAAGAGCTTGGAAACCCGGCTGTG	216	
Db	240	CATCAACAACTCAAAAGGGTTTCCGTCACTCAGATCAAGAGCTTGGAAACCCGGCTGTG	299	
QY	217	GGATGGCGGCTTCTGTAGCCCACTCAGAGGAGACGTTCTTCTTGTGACCAA	276	
Db	300	GGATGGCGGCTTCTGTAGCCCACTCAGAGGAGACGTTCTTCTTGTGACCAA	359	
QY	277	CTTCTTGTGACGCCACCCCAAGTTTCAGGCGAGATGCCAGAGACCCCTCCGTCCTCCAT	336	
Db	360	CTTCTTGTGACGCCACCCCAAGTTTCAGGCGAGATGCCAGAGACCCCTCCGTCCTCCAT	419	
QY	337	GGCTAACTCTGGGTTCAGAGACTGCCCCAAGGGGAGGAGGACACACAGCCACGG	396	
Db	420	GGCTAACTCTGGGTTCAGAGACTGCCCCAAGGGGAGGAGGACACACAGCCACGG	479	
QY	397	TGTAAAAACAGGCCAGTGTGTGTTCATGGGACCCACAGGACCTGTGAGATCTGGAG	456	

Db	480	TGTAATAACAGGCCAGTGTGTGGTGTTCATATGGAGCCACAGACCTGTGAGATCTGGAG	539
Qy	457	TTGGTGGCCAGTGAAGATGGCGTGTGGCTCGAGGCCCTCTGCTGGCCAGGCCAGAA	516
Db	540	TTGGTGGCCCGTGGAGAGTGGCGTGTGGCTCGAGGCCCTCTGCTGGCCAGGCCAGAA	599
Qy	517	CTTCACACTGTTTCATCAAAACACAGTCACTTCAGCAAGTTCAACTTCTCTAACTTCT	576
Db	600	CTTCACACTGTTTCATCAAAACACAGTCACTTCAGCAAGTTCAACTTCTCTAACTTCT	659
Qy	577	TGCTTGGAGACTGGAGCCCACTATTTTAAGCACTGCGCTATGAACCAATTCAG	636
Db	660	TGCTTGGAGACTGGAGCCCACTATTTTAAGCACTGCGCTATGAACCAATTCAG	719
Qy	637	CCCCTACTGCTCCGCTGTTCGCACTGGGACCTCGTGCCCAAGCGCTGGAGGACCTTCCA	696
Db	720	CCCCTACTGCTCCGCTGTTCGCACTGGGACCTCGTGCCCAAGCGCTGGAGGACCTTCCA	779
Qy	697	GGACTGGCGTGTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGGA	756
Db	780	GGACTGGCGTGTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGGA	839
Qy	757	CACCGGGACTCTGGCTGCTGGCTCACTACTCTCCAGTGCAGGAGAGCTACAA	816
Db	840	CACCGGGACTCTGGCTGCTGGCTCACTACTCTCCAGTGCAGGAGAGCTACAA	899
Qy	817	CTTCAGGACAGCCACTCACTGGTGGGAGCAACCGGCTGTGGAGCCCGCACCTGCTCAA	876
Db	900	CTTCAGGACAGCCACTCACTGGTGGGAGCAACCGGCTGTGGAGCCCGCACCTGCTCAA	959
Qy	877	GCTCTATGAATCGCTTCGACATCTCTGTCACCGGACAGGAGGAGTTCGGGCTCAT	936
Db	960	GCTCTATGAATCGCTTCGACATCTCTGTCACCGGACAGGAGGAGTTCGGGCTCAT	1019
Qy	937	CCCAAGCGGCTCACTTGGGACCGGGGAGCTTGGCTGGGCTGTGCTACCTTTTCTG	996
Db	1020	CCCAAGCGGCTCACTTGGGACCGGGGAGCTTGGCTGGGCTGTGCTACCTTTTCTG	1079
Qy	997	TGACTGTCTACTGTGTATGTGATAGAGAGCCATTTCTACTGGAGGACAAAGTATGA	1056
Db	1080	TGACTGTCTACTGTGTATGTGATAGAGAGCCATTTCTACTGGAGGACAAAGTATGA	1139
Qy	1057	GGAGCCAAAGCCCGGAAAGCAACCGCACTCTGTGTGGAGGAGCTGCCCTTGTGATC	1116
Db	1140	GGAGCCAAAGCCCGGAAAGCAACCGCACTCTGTGTGGAGGAGCTGCCCTTGTGATC	1199
Qy	1117	CCAAGCCGACTGGCCGAGTGCCTCAGACGAGCTCAGACCTGCACCCACGCGCACTGC	1176
Db	1200	CCAAGCCGACTGGCCGAGTGCCTCAGACGAGCTCAGACCTGCACCCACGCGCACTGC	1259
Qy	1177	TGCTGGGAGTCAGACACAGACAGGATGSCCTGTCCAGTTCCTGACACCCACTTGC	1236
Db	1260	TGCTGGGAGTCAGACACAGACAGGATGSCCTGTCCAGTTCCTGACACCCACTTGC	1319
Qy	1237	AACCCATTCGGGAGCTGTAGCCGTTCCCTGTCTGTGTGAGTGTGGGGCTGGAGAGG	1296
Db	1320	AACCCATTCGGGAGCTGTAGCCGTTCCCTGTCTGTGTGAGTGTGGGGCTGGAGAGG	1379
Qy	1297	CGGGCCCTGCTGGGATCTCAGAGATGAGCCCGCAGCATGGAGGATTTGGGGTAGAAT	1356
Db	1380	CGGGCCCTGCTGGGATTTCAAGGATGAGCCCGCAGCATGGAGGATTTGGGGTAGAAT	1439
Qy	1357	TCCACCTTGAACCCAGCAGACAGTCCCTCCCTGTACTCCACCTTGTGTAGGGTGTGC	1416
Db	1440	TCCACCTTGAACCCAGCAGACAGTCCCTCCCTGTACTCCACCTTGTGTAGGGTGTGC	1499
Qy	1417	CTCAGGAGCCATAGAACTCGGCTGTGTTTGTAGACGCGGACAGAACTGTACCCGTGGAG	1476
Db	1500	CTCAGGAGCCATAGAACTCGGCTGTGTTTGTAGACGCGGACAGAACTGTACCCGTGGAG	1559
Qy	1477	ACTGGGAGCCAGCAGGACCTGTATTGAGGGCTCCGACTGCATGTGGCAGGGGCTC	1536
Db	1560	ACTGGGAGCCAGCAGGACCTGTATTGAGGGCTCCGACTGCATGTGGCAGGGGCTC	1619

Qy	1537	CTGCTGCTCTGGGCTGGAGTCTCTCTCCAGTGTCTGTCTCCAGTGTCTCTAGCAG	1596
Db	1620	CTGCTGCTCTGGGCTGGAGTCTCTCTCCAGTGTCTGTCTCCAGTGTCTCTAGCAG	1679
Qy	1597	AGGTATGCTTACCAGCTG	1614
Db	1680	AGGTATGCTTACCAGCTG	1697

RESULT 2

US-09-191-136-30

; Sequence 30, Application US/09191136B

; Patent No. 6214581

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Lynch, Kevin J.

; APPLICANT: Burgard, Edward C.

; APPLICANT: Van Biesen, T.

; TITLE OF INVENTION: Nucleic Acids Encoding A Functional

; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production

; TITLE OF INVENTION: And Use Thereof

; FILE REFERENCE: 6293.US.P1

; CURRENT APPLICATION NUMBER: US/09/191,136B

; CURRENT FILING DATE: 1998-11-13

; EARLIER APPLICATION NUMBER: US 09/008,526

; EARLIER FILING DATE: 1998-01-16

; EARLIER APPLICATION NUMBER: US 09/008,185

; EARLIER FILING DATE: 1998-01-16

; EARLIER APPLICATION NUMBER: US 60/071,298

; EARLIER FILING DATE: 1998-01-16

; EARLIER APPLICATION NUMBER: US 60/071,669

; EARLIER FILING DATE: 1998-01-16

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30

; LENGTH: 1360

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequencing Primer (polynucleotide)

US-09-191-136-30

Query Match 43.2%; Score 1162.4; DB 3; Length 1360;

Best Local Similarity 99.9%; Pred. No. 1.1e-288;

Matches 1163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	97	GTGGCTCTCTCGCCAAAAGGCTACAGGAGCGGACCTGGAAACCCAGTTTCCAT	156
Db	180	GTGGCGCTCTCTCGCCAAAAGGCTACAGGAGCGGACCTGGAAACCCAGTTTCCAT	239
Qy	157	CATCACCAACTCAAGGGGTTTCGTCACATCAAGGAGCTTGGAAACCCGCTGTG	216
Db	240	CATCACCAACTCAAGGGGTTTCGTCACATCAAGGAGCTTGGAAACCCGCTGTG	299
Qy	217	GGATGGCCGACTTCGTGAAGCCACCTCAGGAGAGAACGTGTTCTTTGGTGACCA	276
Db	300	GGATGGCCGACTTCGTGAAGCCACCTCAGGAGAGAACGTGTTCTTTGGTGACCA	359
Qy	277	CTTCTCTGTGACCCAGCCCAAGTTTCAGGCGAGATGCCAGAGCACCCGCTCCCTCACT	336
Db	360	CTTCTCTGTGACCCAGCCCAAGTTTCAGGCGAGATGCCAGAGCACCCGCTCCCTCACT	419
Qy	337	GGCTAACTGCTGGGTGAGAGGACTGCCCGAAGGGAGGAGGACACACAGCCACGG	396
Db	420	GGCTAACTGCTGGGTGAGAGGACTGCCCGAAGGGAGGAGGACACACAGCCACGG	479
Qy	397	TGTAAACAGCCAGTGTGTGTTCAATGGGACCCACAGGACCTGTGAGATCTGGAG	456
Db	480	TGTAAACAGCCAGTGTGTGTTCAATGGGACCCACAGGACCTGTGAGATCTGGAG	539
Qy	457	TTGGTGCCCACTGGAGTGGCGTTGTGCCCTTCGAGGCCCTGTGTGGCCAGGCCAGAA	516

Db	1095	GGAGGCCAAGGCCCCGAAAGCAACGCCCAACTCTCTGTGTGGAGGGAGCTGGGCCCTTGCATC	1154
Qy	1117	CAAGGCCCACTGGCGAGTGCTCAGACGGAGCTCAGCACTGTGCACCCACGGCCACTGC	1176
Db	1155	CNAGGCCCACTGGCCGAGTGCTCAGACGGAGCTCAGCACTGCACCCACGGCCACTGC	1214
Qy	1177	TGCTGGGAGTCTGACACAGACACCAACGAGTGGCCCTGTCAAAGTTCTGACCCCACTTGCC	1236
Db	1215	TGCTGGGAGTCTGACACAGACACCAACGAGTGGCCCTGTCAAAGTTCTGACCCCACTTGCC	1274
Qy	1237	AACCCATTCCGGAGCCTG	1255
Db	1275	AACCCATTCCGGAGCCTG	1293

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RESULT 4
US-09-191-136-28
; Sequence 28, Application US/09191136B
; Patent No. 6214581
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding A Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
; TITLE OF INVENTION: And Use Thereof
; FILE REFERENCE: 6293.US.P1
; CURRENT APPLICATION NUMBER: US/09/191,136B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 09/008,536
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 09/008,185
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,298
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,669
; EARLIER FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequencing Primer
US-09-191-136-28

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Db 301 TGACAGACAGACAGAGTGGCCCTGCTCCAAAGTTCTGCACACCACTTGCACCAACCAATTC 360

QY 1246 CGGAGCCTGTAGCGGTTCCCTGCTGTTGAGAGTT 1281

Db 361 CGGAGCCTGTAGCGGTTCCCTGCTGTTGAGAATT 396

RESULT 5

US-09-016-434-831

; Sequence 831, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSER: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCES/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 831:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1750 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: SCORNOT01

; CLONE: 555697

; US-09-016-434-831

	Query Match	8.9%;	Score 239.2;	DB 4;	Length 1750;
	Best Local Similarity	56.3%;	Pred. No. 1.8e-51;		
	Matches 529;	Conservative 0;	Mismatches 378;	Indels 33;	Gaps 33
QY	152	TCATCATCCCAACTCAAGGGGTTTCGTCACTCAGATCAAGGAGCTTCGGAACCGG	211		
DB	214	TCCGTTACGACCAAGGTCAGGGCGTGGTACCAACTCTTAACTTGGATTCGG	273		
QY	212	CTGTGGGATGTGGCGCAGCTTCGTGAAGCCACCTCAGGGAGAGAACTGTTCTTTGTGG	271		
DB	274	ATCTGGGATGTGGCGGATTATGTATACCAGCTCAGGAGGAAACTCCCTCTTCGTCATG	333		
QY	272	ACCAATCTCTTTGTGACGCCAGCCCAAGTTTCAGGGCAGATGCCCAGAGACACCGGTCGGTC	331		
DB	334	ACCAACGTGATCTCCATCCATGAACACAGACACGGGGCTGTGCCCGAGATTC---CAGAT	390		
QY	332	CCACTGGGCTAACTGTGTGGTGCAGCAGGATGTCGCCCGAAGGGGAGGGAGGCACACACAGC	391		

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Db 391 GCGACACTGTGTGTAATCAGATGCCAGTGTACTGCGGGTCTGCGGACCCACAGC 450
Qy 392 CACGGTGTAAACAGAGCCAGTGTGTGTTCAATGGACCCACAGGACCTGTGAGATC 451
Db 451 AACGGAGTCTCAACAGGAGTGTGCTAGCTTTCAACGGGTGCTCAAGACGTGTGAGGTG 510
Qy 452 TGGAGTTGGTGCCAGTGTGAGAGTGGC---GTTGTGCCCTCAGAGCCCTGCTGCCCCAG 508
Db 511 GCGGCTGTGTGCGGTGGAGATGACACACAGGTGCCACACCTGCTTTTAAAGGCT 570
Qy 509 GCGCAGAACTTCACTGTTCATCAAAACACACAGTCACTTCAGCAAGTTCAACTTCTCT 568
Db 571 GCAGAAAATTCACCTCTTTGGTTAAGAACACATCTGGTATCCCAATTTAATTTGAGC 630
Qy 569 AAGTCCAAATGCTTGGAGACCTGGGACCCACCTATTTAAGCACTGCGCTATGAACA 628
Db 631 AAGAGGAATATCTTCCCAACATCACCATCTTACCTCAAGTCGTGATTTATGATGCT 690
Qy 629 CAATTGAGCCCTACTGTCCCGTGTTCGGCAATGGGACCTCGTGGCCAAAGCTGGAGG 688
Db 691 AAAACAGATCCCTTCTGCCCATATTCGTCCTTGGCAAAATAGTGGAGACGAGGACAC 750
Qy 689 ACCTTCGAGGACCTGGCTGTGCTGGTGTCTGTAGGATCAGAGTTCACTGGGATTTGT 748
Db 751 AGTTTCCAGGACATGCCGTGGAGGAGGCATCATGGGCATCCAGSTCAACTGGGACTGC 810
Qy 749 GACCTGGACACCGGAGACTCTGGCTGTGGCTCTACTCTCTCCAGTCCAGTGCAGGAGA-- 806
Db 811 AACCTGGACAGAGCGCCCTCTGCTGTGGCAGGTACTCTTCCGCGCTCGATACA 870
Qy 807 -----AGACTACAACTTCAGGACAGCCACTCACTGTGGTGG 841
Db 871 CGGAGCTGTAGCACAAAGTATCTCTGCTGCTACAAATTCAGGTTTGCAGTACTACAGA 930
Qy 842 GAGCAACCGGTGTGAGCGCCGACCTGCTCAGCTCTATGATCGGTTCGACATC 901
Db 931 GACCTGGCTGGCAAGAGAGCGACGCTCATCAAGGCTATGGCATCCGCTTCGACATC 990
Qy 902 CTCGTACCGGAGCAGGAGGAAGTTTCGGGTCTATCCCGCGCTCACACTGGGCAAC 961
Db 991 ATTGTGTTGGAGGAGGAGAAATTCACATCATCCCCCATATGATCAACATCGGCTCT 1050
Qy 962 GGGCAGCTGTGGTGGGTGTGCTACCTTTTCTGTGACCTGTCTACTCTGTATGTGGAT 1021
Db 1051 GGCCTGGCAGCTGTAGGATGCGACCGTGTGTGTGACATCATAGTCTCTACTGCAATG 1110
Qy 1022 AGAGAAGCCCATTTCTACTGGAGGACAAAGTATGAGGAGG 1061
Db 1111 AAGAAAGACTCTACTATCGGAGAGAAATATAATATG 1150
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RESULT 6

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US-08-742-621-2
; Sequence 2, Application US/08742621
; Patent No. 5856129
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: COLEMAN, ROGER
; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,621
; FILING DATE: Filled Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0147 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: CONSENSUS
; CLONE: -742-621-2
; US-08-742-621-2
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Query Match 8.9%; Score 239.2; DB 2; Length 1762;
Best Local Similarity 56.3%; Pred. No. 1.8e-51;
Matches 529; Conservative 0; Mismatches 378; Indels 33; Gaps 3;

Qy 152 TCATCATCAACCAAACTCAAAAGGGTTTCGTCATCAGATCAAGAGGCTTGGAAACCGG 211
Db 214 TCGGTACGACCAAGTCAAGGCGTGGTGTGACCAACACTTCTAAACTTGGATTCGG 273
Qy 212 CTGTGGAGTGTGCCCACTTCGTGAAGCCACTCAGGAGAGAACGTGTCTTCTTGGTG 271
Db 274 ATCTGGATGTGGCGGATTATGTATCCAGCTCAGGAGGAAACTCCCTCTTTCGTATG 333
Qy 272 ACCAACTTCTGTGACGCGCAGCCCAAGTTCAAGGCGAGATGCCAGAGACACCGCTCCGTC 331
Db 334 ACCAAGTGTATCTCTACCATGAACACAGACAGGGGCTGTGCCCGAGATTC---CAGAT 390
Qy 332 CCACTGGCTAACTGTGTGGTTCGACGAGGACTGCCCGAAGGGGAGGAGGACACACAGC 391
Db 391 GCACCACTGTGTGTAATCAGATGCCAGTCTACTSCGGGTCTGCCGACCCACACAGC 450
Qy 392 CACGGTGTAAACAGCCAGCTGTGTGTTCAATGGGACCCACAGGACCTGTGAGATC 451
Db 451 AACGGAGTCTCAACAGGAGGTCGTAGCTTTCAACGGGTCCGTCAAGACGTGTGAGGTG 510
Qy 452 TGGAGTTGGTGCCCACTGTGAGAGTGGC---GTTGTGCCCTCGAGGCCCTGTGGCCCGAG 508
Db 511 GCGGCTGTGTGCCCGTGGAGGATGACACACAGTGCACCAACTCTTTTAAAGGCT 570
Qy 509 GCCCAGAACTTCACTGTTCATCAAAACACAGTCACTTCAGGAGTTCACCTCTCT 568
Db 571 GCAGAAAATTCACCTCTTTTGGTTAAGAACACATCTGATATCCCAATTTAATTTGAGC 630
Qy 569 AAGTCCAAATGCTTGGAGACCTGGGACCCCACTATTTTAAAGCACTGCGCTATGAACA 628
Db 631 AAGAGGAATATCTTCCCAACATCACCATCTACTTCAAGTCGTGCTATTTATGATGCT 690
Qy 629 CAATTGAGCCCTACTGTCCCGTGTTCGGCATTTGGGACCTGTGCCCAAGGCTGGAGG 688
Db 691 AAAACAGATCCCTTCTGCCCATATTCGCTCTTGGCAAAATAGTGGAGAACGAGGACAC 750
Qy 689 ACCTTCGAGGACCTGGCTGTGCTGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGT 748
Db 751 AGTTTCCAGGACATGCCGTGGAGGAGGCATCATGGGCATCCAGTCACTGGGACTGC 810
Qy 749 GACCTGGACACCGGAGACTCTGTGGCTCTACTCTCTTCCAGTCCAGTGCAGGAGA-- 806
Db 811 AACCTGGACAGAGCGCCCTCTGCTGTGGCAGGTACTCTTCCGCGCTCGATACA 870
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QY 807 -----AGAGCTACAACTTCAGGACAGCCACTCACTGGTG 841
 Db 871 CGGACGCTTGACCAACAGTATCTCTGGGTACAAATTCAGGTTGCCAAGTACTACAGA 930
 QY 842 GAGCAACCGGCTGGAGGCGCCGACCTCTCAAGCTCTATGGAATCCCGCTTCGACATC 901
 Db 931 GACTGGCTGCAACAGGACGCGACGCTCATCAAGCCCTATGGCATCCGCTTCGACATC 990
 QY 902 CTCGTACCGGCGAGGACGGAAGTTTCGGGCTCATCCCGACGCGCTGCACACTGGGACC 961
 Db 991 ATTGTGTTTGGGAAGGAGGAGAAATTTGACATCATCCCACTATGATCAACATCGGCTCT 1050
 QY 962 GGGGACGCTTGGCTGGGCGTGTCACTTTTCTGTGACCTGTCTACTGCTGTATGTTGGAT 1021
 Db 1051 GGCCTGGACCTGTAGGATGGGACGCTGTGTGTGACATCATAGTCTCTACTGCTATG 1110
 QY 1022 AGAGAAGCCCACTTTCTACTGAGGACAAAGTATGAGGAGG 1061
 Db 1111 AAGAAAGACTCTACTATCGGAGAGAAATATAATATG 1150

RESULT 7

US-09-191-608-21
 ; Sequence 21, Application US/09191608
 ; Patent No. 6242216
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynch, Kevin J.
 ; APPLICANT: Burgard, Edward C.
 ; APPLICANT: Metzger, Randy E.
 ; APPLICANT: Niforatos, Wendie
 ; APPLICANT: Touma, Edward B.
 ; APPLICANT: Van Biesen, T.
 ; TITLE OF INVENTION: Nucleic Acids Encoding a Functional
 ; TITLE OF INVENTION: Human Purinoceptor P2X2 and P2X4 And Methods Of Production
 ; TITLE OF INVENTION: And Use Thereof
 ; FILE REFERENCE: 6394.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/191,608
 ; CURRENT FILING DATE: 1998-11-13
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 1206
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-191-608-21

Query Match 8.8%; Score 237.6; DB 3; Length 1206;
 Best Local Similarity 56.2%; Pred No. 3.9e-51;
 Matches 528; Conservative 0; Mismatches 379; Indels 33; Gaps 3;
 QY 152 TCATCATCAAACTCAAGGGTTTCCTGCTACTAGATCAAGGAGCTTGGAAACCGG 211
 Db 207 TCCGTTAGCAACAGGTCAGGGGCTGTGTGACCAACACTTCTAAACITGGATTCCGG 266
 QY 212 CTGCTGGATGGCCGACTTGTGAAGCCACTCAGGAGAGACGTTCTTCTTCTGGTG 271
 Db 267 ATCTGGATGTGGCGGATATGTGATACAGCTCAGGAGAACTCCCTCTGCTCATG 326
 QY 272 ACCAACTTCTTGTGACGCCAGCCCAAGTTTCAGGCGAGATCCCGAGACCCCTCCGTC 331
 Db 327 ACCAAGTGATCTCTCAACATGAACAGACAGAGGCGCTGTGCCCGAGATTC---CAGAT 383
 QY 332 CACTGGCTAACTCTGGTGCACGAGACTGCCCGAGGGGAGGACACACAGC 391
 Db 384 GCGACCACTGTGTGTAATAGATCCAGCTGTACTCCGCTCTGCGGACCCACAGC 443
 QY 392 CACGCTGTAAACAGGCGAGTGTGTGTTTCAATGGGACCCACAGGACCTGTGAGATC 451
 Db 444 RACGAGCTCAACAGGAGGTCGCTAGCTTTCAACGGTCCGTCAAGACGTGTGAGTG 503
 QY 452 TCGAGTTGGTCCCAAGTGGAGAGTGGC---GTTGTGCCCTCGAGGCCCTCTGCCCCAG 508
 Db 504 GCGGCTGTGTGCCGCTGGAGGATGACACACAGCTGCGCAACCTGTCTTTTAAAGGCT 563

QY 509 GCCAGAACTTCACACTGTTTCATCAAAACACAGTCACCTTCAGCAAGTTCAACTTCTCT 568
 Db 564 GAGAAACTTCACACTGTTTGGTTAAGAAACAATCTGGTATCCCAATTTAAATTTTCAGC 623
 QY 569 AAGTCCAAATGCTTGGAGACCTGGGACCCCACTTATTTAAGCACTGCGGCTATGAACCA 628
 Db 624 AAGAGGAATATCTTCCCAACATCACCACCTACTTACCTCAAGTCTGTCATTTATGATGCT 683
 QY 629 CAATTCACGCTTACTGTCGCTGTTCCGATTTGGGACCTCTGTCGCGCAAGCTGGAGGG 688
 Db 684 AAAACAGATCCCTTCTGCCCATATTTCCGCTTTGGCAAAATAGTGGAGAACGAGGACAC 743
 QY 689 ACCTTCGAGGACCTGGCTTGTGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATGT 748
 Db 744 GCTTCCAGGACATGGCGTGGAGGGAGGCATCATGGGCATCCAGGTCAACTGGGACTGC 803
 QY 749 GACCTGGACACCGGGGACTCTGGCTGGCTGCTCACTACTCTTCCAGCTCGAGGAGA-- 806
 Db 804 AACCTGGACAGAGCCGCTCTCTGCTTGGCCAGGTACTCTTCCGCGGCTCGATACA 863
 QY 807 -----AGAGCTACAACTTCAGGACAGCCACTCACTGGTG 841
 Db 864 CGGACGCTTGACCAACAGTATCTCTGCTTACATTTTCAGTTTGGCAAGTACTACAGA 923
 QY 842 GAGCAACCGGCTGGAGGCGCCGACCTGCTCAAGCTCTATGGAATCCGCTTCGACATC 901
 Db 924 GACCTGGCTGGCAACGAGCAGCGCCTCATCAAGGCTATGGCATCCGCTTCGACATC 983
 QY 902 CTCGTACCGGCGAGGAGGAGTTCCGGCTCATCCCGCGCTCATCCCACTATGATCAATCGGCTCT 961
 Db 984 ATGTGTTTGGAGCGAGGAAATTTGACATCATCCCACTATGATCAATCGGCTCT 1043
 QY 962 GGGGACGCTTGGCTGGGCTGCTCACTTTTCTGTGACCTGCTACTCTCTGTATGATG 1021
 Db 1044 GCGCTGGCACTGCTAGGATGGGACCGCTGTGTGACATCATAGTCTCTACTGCTATG 1103
 QY 1022 AGAGAAGCCCACTTCTACTGAGGACAAAGTATGAGGAGG 1061
 Db 1104 AAGAAAGACTCTACTTACTGCGGAGAGAAATATAATATG 1143

RESULT 8

US-08-750-134A-10
 ; Sequence 10, Application US/08750134A
 ; Patent No. 5985603
 ; GENERAL INFORMATION:
 ; APPLICANT: VALERA, SOLEDAD
 ; APPLICANT: BUELL, GARY
 ; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/750,134A
 ; FILING DATE: 22-JAN-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CRAWFORD, ARTHUR C.
 ; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 1430-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4006

TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-750-134A-10

Query Match 8.7%; Score 233.4; DB 2; Length 2643;
Best Local Similarity 56.7%; Pred. No. 6.9e-50;
Matches 526; Conservative 0; Mismatches 371; Indels 30; Gaps 4;

QY 164 AAATCAAGGGGTTCCGTCTCATGATCAAGAGCTTGAAACCGGCTGTGGATGTG 223
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QY 375 AAATCAAGGGGCTGGCGTCAACAGCTCCCTGGCGTGGCCCGGCTGGGATGTG 434
Db |||||
QY 224 GCCGACTTCGTGAAGCCCTCAGGAGAGACGTTCTCTTGGTGACCACTTCCTT 283
Db |||||
QY 435 GCTGACTAGCTTCCAGCCCGAGGGGACAACTCCCTTGGTGATGACCAATTCATC 494
Db |||||
QY 284 GTGACCCAGCCCAAGTTGAGGCGAGATGCCAGAGCACCGGTCCCTGCTTAAC 343
Db |||||
QY 495 GTGACCCCGAAGCAGACTCAAGGCTACTGCGCAGAGCACCC-----AGAAGGGGGCATA 548
Db |||||
QY 344 TGCTGGTTCGACGAGACTGCCCGAAGGGGAGGAGGCACACAGCCACGGTGTAAAA 403
Db |||||
QY 549 TCGAAGGAAGCAGTGGCTGTACCCCTGGGAAGGCCAAGAGAGGCGCCAGGCGATCGC 608
Db |||||
QY 404 ACAGCCGAGTGTGGTGTTCATATGGGACCCACAGAGCTGTGAGATCTGGAGTTGGTG 463
Db |||||
QY 609 ACGGCAAGTGTGGCTTCAACGACACTGTGAAGCTGTGAGATCTTTGGCTGGTG 668
Db |||||
QY 464 CAGTGGAGAGTGGCTTGTGCCCTCGAGGC---CCCTGTGGCCCGCCGCGCCAGAACTTC 520
Db |||||
QY 669 CCGTGGAGTGGATGACGACATCCCGCGCCCTGCGCTTCTCCGAGAGCGCCGAGAACTTC 728
Db |||||
QY 521 ACACGTGTTTCATCAAAACACAGTCACTTCAGCAAGTTCACTTCTTAAGTCAATGCC 580
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QY 729 ACTCTTTTCATCAAGAACAGCATGAGCTTCCAGCTTCAAGGTCAAGCGGCAACCTG 788
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QY 581 TTGAGAGCTGGGACCCCACTTATTTAAGCACTGCCCTATGAACCAATTCAGCCCC 640
Db |||||
QY 789 GTGAGGAGTGAATGCTGCCACATGAAGACTGCTCTTTCAAGACCTGCAACCCC 848
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QY 641 TACTGTCCTGGCTTCCGATTTGGGACCTCGTGGCCAGGCTGGAGGACCTTCAGGAC 700
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QY 849 CTGTGCCAGCTTCCAGCTTGGCTACGTTGGTGAAGAGTCAGGCGCAACTTCAGCAC 908
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QY 701 CTGGCGTTGCTGGGTGGCTCTGTAGGCATCAGATTCATCTGGGATTTGACCTGGACAC 760
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QY 909 CTGGCTGAGAGGGTGGAGTGGTGGCATCACCATCGACTGSCACTGTGACTGGACTGG 968
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QY 761 GGGGACTCTGGTGTGGCGCTCACTATCTCTTCAGCTGCGAGGAGA----- 809
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QY 969 CAGCTACGCGCACTGAGACCCATCTATGAGTTCCATGGGCTGTACGAGAGAAAAATCTC 1028
Db |||||
QY 810 -----GCTACAACTTCAGAGACCCACTCACTGGTGGGAGCAACCGGTGTGGAGGCC 862
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QY 1029 TCCCGAGGCTTCACTTCAAGTTTCCAGGACACTTTTGGAGAC---GGACCAACTAC 1085
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QY 863 CGCACCTGCTCAAGCTCATGGAAATCCGCTTCGACATCTCTGTCACCGGCGAGCGAGG 922
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QY 1086 CGTCACTCTTCAAGGTGTTGGGATTCGCTTTGACATCTCTGTTGGAGCGGCAAGCGCGG 1145
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QY 923 AAGTTCGGGCTCATCCCGAGCGCTGCACACTGGGCGAGCGGCGAGCTTGGCTGGGGTG 982
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QY 1146 AAGTTTGACATCATCCCTCAATGACCACTACCTGGCTCTGGAATTTGGATCTTTGGGGTG 1205
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QY 983 GTCACTTTTCTGTGACCTGCTACTGCTGTATGTGATAGAGAGGCCAATTTCTACTGG 1042
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QY 1206 GCCACAGTTCTGTGACCTGCTGCTTTCACATCTCTGCTTAAGAGGCACTACTACAAG 1265
Db |||||

QY 1043 AGGACAAAGTATGAGGAGGCCAAGGCC 1069
Db |||||
QY 1266 CAGAAGAAGTTCAAATACGCTGAGGAC 1292
Db |||||

RESULT 9
US-09-363-745-10
; Sequence 10, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-363-745-10

Query Match 8.7%; Score 233.4; DB 3; Length 2643;
Best Local Similarity 56.7%; Pred. No. 6.9e-50;
Matches 526; Conservative 0; Mismatches 371; Indels 30; Gaps 4;

QY 164 AAATCAAGGGGTTTCGTCTCATGATCAAGAGCTTGAAACCGGCTGTGGATGTG 223
Db |||||
QY 375 AAATCAAGGGGCTGGCGTCAACAGCTCCCTGGCGTGGCCCGGCTGGGATGTG 434
Db |||||
QY 224 GCCGACTTCGTGAAGCCACCTCAGGAGAGAACGTTCTTCTTGGTGACCAACTTCCTT 283
Db |||||
QY 435 GCTGACTAGCTTCCAGCCCGAGGGGACAACTCCCTTGGTGATGACCAATTCATC 494
Db |||||
QY 284 GTGACCCAGCCCAAGTTGAGGCGAGATGCCAGAGCACCGGTCCCTGCTTAAC 343
Db |||||
QY 495 GTGACCCCGAAGCAGACTCAAGGCTACTGCGCAGAGCACCC-----AGAAGGGGGCATA 548
Db |||||
QY 344 TGCTGGTTCGACGAGACTGCCCGAAGGGGAGGAGGCACACAGCCACGGTGTAAAA 403
Db |||||
QY 549 TCGAAGGAAGCAGTGGCTGTACCCCTGGGAAGGCCAAGAGAGGCGCCAGGCGATCGC 608
Db |||||
QY 404 ACAGCCGAGTGTGGTGTTCATATGGGACCCACAGAGCTGTGAGATCTGGAGTTGGTG 463
Db |||||
QY 609 ACGGCAAGTGTGGCTTCAACGACACTGTGAAGCTGTGAGATCTTTGGCTGGTG 668
Db |||||
QY 464 CAGTGGAGAGTGGCTTGTGCCCTCGAGGC---CCCTGTGGCCCGCCGCGCCAGAACTTC 520
Db |||||
QY 669 CCGTGGAGTGGATGACGACATCCCGCGCCCTGCGCTTCTCCGAGAGCGCCGAGAACTTC 728
Db |||||
QY 521 ACACGTGTTTCATCAAAACACAGTCACTTCAGCAAGTTCACTTCTTAAGTCAATGCC 580
Db |||||
QY 729 ACTCTTTTCATCAAGAACAGCATGAGCTTCCAGCTTCAAGGTCAAGCGGCAACCTG 788
Db |||||
QY 581 TTGAGAGCTGGGACCCCACTTATTTAAGCACTGCCCTATGAACCAATTCAGCCCC 640
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QY 789 GTGAGGAGTGAATGCTGCCACATGAAGACTGCTCTTTCAAGACCTGCAACCCC 848
Db |||||
QY 641 TACTGTCCTGGCTTCCGATTTGGGACCTCGTGGCCAGGCTGGAGGACCTTCAGGAC 700
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QY 701 CTGGCGTTGCTGGGTGGCTCTGTAGGCATCAGATTCATCTGGGATTTGACCTGGACAC 760
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QY 909 CTGGCTGAGAGGGTGGAGTGGTGGCATCACCATCGACTGSCACTGTGACTGGACTGG 968
Db |||||
QY 761 GGGGACTCTGGTGTGGCGCTCACTATCTCTTCAGCTGCGAGGAGA----- 809
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QY 969 CAGCTACGCGCACTGAGACCCATCTATGAGTTCCATGGGCTGTACGAGAGAAAAATCTC 1028
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QY 810 -----GCTACAACTTCAGAGACCCACTCACTGGTGGGAGCAACCGGTGTGGAGGCC 862
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Db |||||
QY 863 CGCACCTGCTCAAGCTCATGGAAATCCGCTTCGACATCTCTGTCACCGGCGAGCGAGG 922
Db |||||
QY 1086 CGTCACTCTTCAAGGTGTTGGGATTCGCTTTGACATCTCTGTTGGAGCGGCAAGCGCGG 1145
Db |||||
QY 923 AAGTTCGGGCTCATCCCGAGCGCTGCACACTGGGCGAGCGGCGAGCTTGGCTGGGGTG 982
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QY 1146 AAGTTTGACATCATCCCTCAATGACCACTACCTGGCTCTGGAATTTGGATCTTTGGGGTG 1205
Db |||||
QY 983 GTCACTTTTCTGTGACCTGCTACTGCTGTATGTGATAGAGAGGCCAATTTCTACTGG 1042
Db |||||
QY 1206 GCCACAGTTCTGTGACCTGCTGCTTTCACATCTCTGCTTAAGAGGCACTACTACAAG 1265
Db |||||

QY 464 CCAGTGGAGAGTGGCGTTGTGCTCCGAGG-CCCTGCTGGCCAGGCCAGAACTTC 520
DB 669 CCCGTGGAGTGGATGACGACATCCCGCGCCCTGCTCCGAGAGCGGAGAACTTC 728
QY 521 ACATGTTTCATCAAAACACAGTACCTTCAGCAAGTTCATCTCTTAAGTCCAAATGCC 580
DB 729 ACTCTTTTCATCAAGAACAGATCAGCTTTCCAGCGTTCAAGTCAACAGCGCGCAACTG 788
QY 581 TTGAGACCTGGAGCCCGACCTATTTAAGCACTGCGCTATGAACACAAATTCAGCCCC 640
DB 789 GTGAGGAGGTGAATGCTGCCCAATGAGACCTGCTCTTTCAAGACCTTCAGCCCC 848
QY 641 TACTGTCCCGTTCCGATTTGGGACCTCTGTCGCAAGCTGAGGAGCTTCGAGGAC 700
DB 849 CTGTGCCAGTCTTCCAGCTTGGCTACGTGTGCAAGAGTCAAGGCGCAACTTCAGCACC 908
QY 701 CTGGCTTCTGGTGGCTCTGTAGGATCAGATTCACCTGGATTCGACCTGGACACC 760
DB 909 CTGGCTGAGAGGGTGGAGTGGTGGATCACCATCGACTGGCACTGTGACCTGGACTGG 968
QY 761 GGGGACTCTGGCTGGCTCTACTCTCTTCCAGCTGAGGAGAGA----- 809
DB 969 CACGTACGGCACTGACAGCCCATCTATGAGTTCCATGGCTGTACGAAGAGAAATCTC 1028
QY 810 -----GCTACAACTTCAGGACGCACTACTCTGTTGGGAGCAACCGGTTGGAGGCC 862
DB 1029 TCCCGAGGCTTCACTTCAAGTTCGAGGCACTTGTGAGAAC-----GGGACCACTAC 1085
QY 863 CGCACCTCTCAAGCTCTATGGAATCGCTTCGACATCTCTGTCACCGGCGAGGAGGG 922
DB 1086 CGTCACTCTCAAGTCTTGGATTCGCTTTCACATCTCTGTTGGAGCGCAAGCGCGG 1145
QY 923 AAGTTCGGGCTCATCCCAAGCGCTGACACTGGGCAACCGGCGAGCTTGGCTGGGGCTG 982
DB 1146 AAGTTGACATCATCCCTACAAATGACCACCATCGGCTCTGGAATGGAATCTTTGGGGTG 1205
QY 983 GTCACTTTTCTGTGACCTCTACTCTGTATGTGATAGAGAGCCCAATTTCTACTGG 1042
DB 1206 GCCACAGTCTCTGTGACCTCTGCTGTTCAATCTGCTTAGAGGCACTACTACAAG 1265
QY 1043 AGGACAAAGTATGAGGCGCAAGGCC 1069
DB 1266 CAGAAGAGATTCAAATACGCTGAGGAC 1292

RESULT 10
US-09-023-655-897
; Sequence 897, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 897:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1166437
; US-09-023-655-897
Query Match 8.7%; Score 233.4; DB 4; Length 2643;
Best Local Similarity 56.7%; Pred. No. 6.9e-50;
Matches 526; Conservative 0; Mismatches 371; Indels 30; Gaps 4;
QY 164 AAATCAAGGGGTTTCGTCATCAGATCAAGAGCTTGGAAACCGGCTGTGGATGTG 223
DB 375 AAATCAAGGGGCTGGCGGTGACCCAGCTCCCTCGCCCTCGCCCGCCAGGTCTGGATGTG 434
QY 224 GCGCACTTCGTGAAGCCACCTCAGGAGAGAAAGTTCCTTCTTGGTGACCACTTCCTT 283
DB 435 GCTGACTAGTCTTCCAGCCAGGGGAGCAACTCTCTTCTGTTGTCATGACCAATTTTCATC 494
QY 284 GTGACCGCAGCCCAAGTTTCAGGGCAGATGCCAGAGACACCCGTCGTCCTCCACTGGCTAAC 343
DB 495 GTGACCCCGAAGCAGACTCAAGGCTACTGCGCAGAGCACCC-----AGAAGGGGGGATA 548
QY 344 TCTCGGTGTCAGGAGTCTCCCGAAGGGGAGGAGGACACACACGCGGTGTAAAC 403
DB 549 TCAAGGAAGACAGTGGCTGTACCCCTGGGAAGGCCAAGAGAGGCCCAAGGATCCGC 608
QY 404 ACAGGCCAGTGTGTGTTTCAATGGGACCCACAGGACCTGTGAGATCTGAGTTGGTGC 463
DB 609 ACGGCAAGTGTGTGGCTTCAACGACACTGTGAAGACGTGTGAGATCTTTGGCTGTGTC 668
QY 464 CCAGTGGAGAGTGGCGTTGTGCTCCGAGG-CCCTGCTGGCCAGGCCAGAACTTC 520
DB 669 CCCGTGGAGTGGATGACGACATCCCGCGCCCTGCTCCGAGAGCGCGAGAACTTC 728
QY 521 ACATGTTTCATCAAAACACAGTCACTCTCAGCAAGTTCAACTCTCTTAAGTCCAAATGCC 580
DB 729 ACTCTTTTCATCAAGAACAGATCAGCTTCCAGCTTCAAGTCAACAGCGCGCAACTG 788
QY 581 TTGAGACCTGGAGCCCGACCTATTTAAGCACTGCGCTATGAACACAAATTCAGCCCC 640
DB 789 GTGAGGAGGTGAATGCTGTCGCCACATGAAGACCTGCTCTTTTCAAGACCCCTGCACCCC 848
QY 641 TACTGTCCCGTTTCGCAATTTGGGACCTCTGTCGCAAGGCTGAGGAGCACTTCGAGGAC 700
DB 849 CTGTGCCAGTCTTCCAGCTTGGCTACGTGTGCAAGAGTCAAGGCGCAACTTCAGCACC 908
QY 701 CTGGCTTCTGGTGGCTCTGTAGGATCAGATTCACCTGGATTCGACCTGGACACC 760
DB 909 CTGGCTGAGAGGGTGGAGTGGTGGATCACCATCGACTGGCACTGTGACCTGGACTGG 968
QY 761 GGGGACTCTGGCTGGCTCTACTCTCTTCCAGCTGAGGAGAGA----- 809
DB 969 CACGTACGGCACTGACAGCCCATCTATGAGTTCCATGGCTGTACGAAGAGAAATCTC 1028
QY 810 -----GCTACAACTTCAGGACGCACTACTCTGTTGGGAGCAACCGGTTGGAGGCC 862
DB 1029 TCCCGAGGCTTCACTTCAAGTTCGAGGCACTTGTGAGAAC-----GGGACCACTAC 1085

QY 863 GCACCCCTGCTCAAGCTCTATGGAAATCGCTTGGACATCTCTCGTCAACCGGCGCAGCAGG 922
Db 1086 CGTCACTCTTCAAGGTGTTTGGATTCGCTTTGACATCTCTGGTGGACGCAAGCCCGG 1145
QY 923 AAGTTGGGCTCATCCCAAGCGCTGCTACACTGGGCGCAGGAGCTTGGCTGGGCTG 982
Db 1146 AAGTTGGATCATCTTACATGACCACTCGCTCTGGAATTGGCATCTTTGGGGTG 1205
QY 983 GTCACTTTTCTGTGACCTGCTACTGCTGTATGTGGAATAGAGAACCCATTTCTACTGG 1042
Db 1206 GCCACAGTTCTGTGACCTGCTGTGCTGTCTACATCTCTGCTTAAGAGGCACTACTACAAG 1265
QY 1043 AGGACAAATATGAGGAGGCGCAAGGCC 1069
Db 1266 CAGAAGAAGTTCAATACGCTGAGGAC 1292

RESULT 11
US-08-750-134A-6
; Sequence 6, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-750-134A-6

Query Match 8.4%; Score 225.4; DB 2; Length 1997;
Best Local Similarity 55.1%; Pred. No. 6.8e-48;
Matches 548; Conservative 0; Mismatches 411; Indels 36; Gaps 4;
QY 97 GTGGGCTCTCTGGCCAAAAGGTTACGAGGAGGAGCTTGGAAACCGGCTGTG 156
Db 235 GTGGGCTCTCTGGGAAAAGGCTTACGAGGAAAAGGACTCCGCTGGTC--AGCTCGGT 291
QY 157 CATCAACAACTCAAGGGGTTCCGCTACTCAGATCAGGAGCTTGGAAACCGGCTGTG 216
Db 292 GACAAACAAAGCAAGGGTGTGGCTGTGACCAACCTCTCAGCTTGGATTCGGATCTG 351
QY 217 GGATGTGGCGACTTCGTGAAGCCACTCAGGAGAGAACGTGTTCTTCTGGTACCAA 276

Db 352 GGACGTGGCGGACTATGTGATTCACGCTCAGGAGGAAAACCTCCCTCTTCATTATGACCAA 411
QY 277 CTTCTTTGTGACCCAGCCCAAGTTTCAAGGCGAGATGCCAGAGCACCCGCTCCGCTCCACT 336
Db 412 CATGATTTGCACCGTGAACCCAGACACAGAGACCTGTCCAGAGATTCT--CTGATAGAC 468
QY 337 GGCTAACTGTGGGTGCACGAGACTGCCCGAAGGGGAGGAGGACACACAGACCCACGG 396
Db 469 CAGCATTTGTAATTCAGACGCCGACTGCACTCTCTGGCTCCGTGGACACCCAGACAGTGG 528
QY 397 TGTAAACAGGCGAGGTGTGTGTTCAATGGGACCCAGAGACTCTGTGAGATCTGGAG 456
Db 529 AGTTGGACTCTGGAAGATGTGTTCTTCAATGAGTCTGTGAAGACCTGTGAGGTGGCTGC 588
QY 457 TTGGTCCCAAGTGGAGAGTGGCGTT--GTGCCCTCGAGGCCCTCTCTGGCCCGACGCCA 513
Db 589 ATGGTCCCGGTGGAGAACGACGTTGGGTGGTGGCCACGCCGGCTTCTTAAAGGCTGCAGA 648
QY 514 GAACTTTCACACTGTTTCATCAAAAACACAGTCACCTTCAGCAAGTTCAACTTCTTAAGTC 573
Db 649 AAACCTTCACTCTTGTGTAAAGAACACATCTGGTATCCCAAGTTTAACTTCAGCAAGAG 708
QY 574 CAATGCTTGGAGACCTGGGACCCCACTTATTTTAAAGCACTCGCGCTATGAACCAATT 633
Db 709 GAACATCTCTCCCAACATACACGCTCTACCTCAAAATCGTGCAATTTACATGCTCAAC 768
QY 634 CAGCCCTACTGTCCCGTGTTCGCGATTTGGGGACCTCTGGCCCAAGGCTGGAGGGACCTT 693
Db 769 GGATCCCTCTGCCCATATTTCCGTTTGGCAATCGTGGGGACGCGGACATAGCTT 828
QY 694 CGAGGACCTGGCGTGTGGTGGCTCTGTAGGACATCAGAGTTCACTGGGATTTGACCT 753
Db 829 CCAGGAGATGGCAGTTGAGGGAGGCATCATGGGTATCCAGATCAAGTGGGACTGCAACCT 888
QY 754 GGACACGGGGACTCTGGCTGTGGCTCACTACTCTCTCCAGCTGCAGGAGAGA---809
Db 889 GGATAGAGCCGCTCTCCCTTTCCTGCCAGATATTCTTCCGGGGCTGCACACCCGGA 948
QY 810 -----GTTCAACTTCAGACAGCCACTCACTGTGGGAGCA 846
Db 949 CTTGGAACACATGTGTCTCTCGCTACAAATTTTCAAGTTTGCCTTACAGGAGACCT 1008
QY 847 ACCGGGTGTGAGGCGCGCACCTGTCTCAGCTCTATGGAATCCGCTTCGACATCTCTCGT 906
Db 1009 GGCGGCAAGAGAGAGCGGCACACTCACCAGGCGTACGGCATCCGCTTTGACATCATCGT 1068
QY 907 CACCGGCGAGCGAGGAAAGTTCCGGGCTCATCCCGCGCGCTCACACTGGGCGCCGCGGC 966
Db 1069 GTTTGGAAGGCTGGGAAGTTTGACATCATCCCTACCATGATCAACGTTGGCTCTGGCTT 1128
QY 967 AGCTTGGCTGGCGTGTGTACCTTTTCTGTGACCTGCTACTCTGTATGTGATAGAGA 1026
Db 1129 GGCGCTCTCGGGTGGCGACGGTGTCTCTGACGTCTATAGTCTCTTACTGATGAAGAA 1188
QY 1027 AGCCCATTTCTACTGGAGGACAAAGTATGAGGAGG 1061
Db 1189 GAAATACTACTACGGGACAAAGATATAAGTATG 1223

RESULT 12
US-09-363-745-6
; Sequence 6, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA

COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/363,745
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/750,134
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAWFORD, ARTHUR C.
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 1430-116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4006
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1997 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-363-745-6

Query Match 8.4%; Score 225.4; DB 3; Length 1997;

Best Local Similarity 55.1%; Pred. No. 6.8e-48; Indels 36; Gaps 4;
Matches 548; Conservative 0; Mismatches 411;

97 GTGGCTCTCTCGCCAAAGGCTACAGAGGGGACCTGGAACCCAGATTTCAT 156
 235 GTGGGTGTTGTTGGGAAAGGGCTACAGAAACGGACTCCGTGTC---AGTCGGT 291
 157 CATCAACAACTCAAGGGTTTCGTCTCAGATCAAGAGCTTGGAACCGGCTGTG 216
 292 GACAAACAAAGCAAGGTGGGTGTGACCAACACCTCTCAGCTTGGAATCCGGATCTG 351
 217 GGATGTGGCCACTTCGTGAAGCCACCTCAGGGAGAGAGCTGTTCTTGTGTGACCA 276
 352 GGAGTGGCGACTATGATGATTCAGCTCAGAGGAAATCCCTCTTCATATGACCAA 411
 277 CTTCTTGTGACGCCAGCCCAAGTTACGGGAGATGCCAGAGCACCCGCTCCCACT 336
 412 CATGATTGTCACTGACCAACAGACAGAGACCTGTCCAGAGATTCTGATTAAGAC 468
 337 GGCTAACTGCTGGTGCAGAGGACTGCCCGAAGGGAGGGAGGACACACAGCCACGG 396
 469 CAGCATTTGTAATTCAGACGCCGACTGCTCTGCTGCTGCTGACACCCACAGCAGTGG 528
 397 TGTAATAACAGCCAGTGTGTGTGTTCAATGGGACCCACAGGACCTGTGAGATCTGGAG 456
 529 AGTTGCGACTGGAAGATGTGTTCTTCAATGAGTCTGTGAAGACCTGTGAGGTGGCTGC 588
 457 TTGTGCGCCAGTGAGAGTGGCGTT---GTGCGCTCAGGCCCTGTGTCGCCACGGCCCA 513
 589 ATGTGTCGCGGTGAGAACACGCTGTGGCGTGCCAAACCGCGGCTTCTTAAAGGCTGAGA 648
 514 GAACTTCACACTGTTCATAAAACACAGTCACCTTCAGCAAGTTCAACTTCTCTAAGTC 573
 649 AACTTTCACCTCTTGTGAAGACACATCTGTGTACCCCAAGTTTAACCTTCAGCAGAG 708
 574 CAATGCTTGGAGACTTGGGACCCCACTATTATTAAGCACTGCGGCTATGAACCAAAAT 633
 709 GAACATCTCTCCCAACATCACCAGCTCTACCTCAATCTGTCATTTACAATGCTCAAA 768
 634 CAGCCCTACTGTCCCGTGTTCGGATTGGGGACCTGTCGCGCAAGGCTGGAGGGACCTT 693
 769 GGATCCCTTCTGCCCCAATATTCGCTTTTGCACAATCTGTGGGAGACCGGGGACATAGCTT 828

694 CGAGGACCTGGCGTTCCTGGTGGCTCTCTAGGCATCAGAGTTCACTGGGATTGTGACCT 753
 829 CCAGGAGATGGCAGATTGAGGGAGGCATCATGGGTATCCAGATCAAGTGGGACTGCAACT 888
 754 GGACACCGGGGACTCTGGGTGCTGGGCTCACTACTCTCTTCCAGCTGCAGGAGAAGA--- 809
 889 GGATAGAGCGGCTCCCTTGGCTGCCAGATATTCCTTCGCGCGCTGGACACCCGGGA 948
 810 -----GCTACAACTTCAGGACGCACTCACTGGTGGGAGCA 846
 949 CTTGGAACACAATGTGTCTCTGGCTTACAAATTCAGGTTTGGCAAGTACTACAGGGA 1008
 847 ACCGGGTGTGGAGCGCCGACCTCTCAAGCTCTATGGAATCCGCTTCGACATCTCGT 906
 1009 GCGCGCAAGAGCAGCGCACACTCACAAAGGCTACGSCATCCGCTTGGACATCATCT 1068
 907 CACCGGCGAGGAGGAAGTTCGGGCTCATCCCAAGCGCGCTCACACTGGGACCGGGGC 966
 1069 GTTTGAAAAGGCTGGGAAGTTTGACATCATCCCTACCATGATCAACGTTGGCTCTGGCTT 1128
 967 AGCTTGGCTGGCGGTGCTCACCTTTTCTGTGACCTGCTACTGCTGTATGTGATAGAGA 1026
 1129 GCGCTCTCGGGGTGGCGACGGTCTCTGTGACGTCTATGCTCTACTGATGATGAGAA 1188
 1027 AGCCCATTTCTACTGGAGGACAAAGTATGAGGAGG 1061
 1189 GAAATACTACTACCGGGACAGAAATATAAGTATG 1223

RESULT 13

US-09-191-608-14
 ; Sequence 14, Application US/09191608
 ; Patent No. 6242216
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynch, Kevin J.
 ; APPLICANT: Burgard, Edward C.
 ; APPLICANT: Metzger, Randy E.
 ; APPLICANT: Niforatos, Wende
 ; APPLICANT: Touma, Edward B.
 ; APPLICANT: Van Biesen, T.
 ; TITLE OF INVENTION: Nucleic Acids Encoding a Functional
 ; TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of Production
 ; FILE REFERENCE: 6394.US.PI
 ; CURRENT APPLICATION NUMBER: US/09/191,608
 ; CURRENT FILING DATE: 1998-11-13
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 1421
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-191-608-14

Query Match 8.0%; Score 214.4; DB 3; Length 1421;
 Best Local Similarity 55.0%; Pred. No. 3.8e-45;
 Matches 553; Conservative 1; Mismatches 407; Indels 45; Gaps 5;

92 GAGAAAGTGGGCTCTCTCGCCAAAAGGCTTACAGGAGCGGGACCTGGAAACCCAGTTT 151
 174 GTGTGGTACGTATTTCATGTCARAAAAGCTTACAGGAGACGAGCGGGCCCGAGAGC 233
 152 TCCATCATCAACAACTCAAAAGGGTTTCCGTCTACTAGATCAGAGAGCTTGGAAACCGG 211
 234 TCCATCATCAACAAAGTCAAGGGATCACCACGTCCGAGACAAAG----- 279
 212 CTGTGGGATGTGGCGGACTTCGTGAAGCCACTCAGGGAGAGAACGTGTTCTTCTTGGTG 271
 280 -TGTTGGAGTGGAGGAGTACGTGAAGCCCCCGAGGGGGGACGGTGTTCAGCATCATC 338
 272 ACCAACTCTTGTGACGCCCAAGTTTCAGGGGAGATGCCAGAGACCCCGTCGTC 331

339 ACCAGGTCGAGGCCACCACTCCAGACACCCAGGACCTGCCCGAGAGCATAAGGGTC 398
332 CCACTGGCTAACTGCTGGTGCAGAGGACTGCCCGAAGGGAGGGAGGCACACAGC 391
339 CACAACGCCACTGCTCTCCGACCCGACTGCTGGGAGCTGGGACATCTGGGA 458
332 CACGGGTAAACACAGGCGAGTGTG---GTGTTCAATGGGACCCACAGACCTGTGAG 448
459 AACGGCTGAGGACCGGGCGTGTGTGCTTATACAGGGGCGCTCCACAGCTGGAG 518
449 ATCTGGAGTGTGTCGCCAGTGGAGAGTGGGTGTGCTGAGGCGCTCTGCTGGCCAG 508
519 GTGTTGGCTGTGTCGCCGTGGAAGATGGGCTCTGTGACCAATTTCTGGGTACGATG 578
509 GCCCAGAACTTACACAGTGTATCAACAAACACAGTCACTTACAGCAAGTTCATCTCT 568
579 GCCCAGAAATTTACCATCTCATCAAGAACAGCATCCACTACCCCAATTTCACTTCTCC 638
569 AAGTCCAAATGCTTGGAGACCTGGACCCCACTATTTTAAAGCATGCGGTATGAACCA 628
639 AAGGGCAACATCGCCGACCGCACAGA---CGGGTACCTGAAGCGCTGCACGTTCCACGAG 695
629 CAATTCAGCCCTACTGTCCTGTTCGCGATTTGGGACCTCGTGCCCAAGGCTGGAGGG 688
696 GCTTCGACCTTACTGCCCCATCTTCAAGCTGGGCTTTATCGTGGAGAGCTGGGGAG 755
689 ACCTTCGAGGACCTGGCGTTGCTGGGTGGCTCTGTAGGCATCAGAGTTCACTGGGAATGT 748
756 ACCTTCAGAGCTCGCACACAGGGTGTGTGTCATCGGGTCAATTAACAGTGGACTGT 815
749 GACCTGGACACCGGGGACTGTGGCTGTGGCTCTACTACTCTTCCASCTGCAGAGAG 808
816 GACCTGGACCTCGCATCGAGTGCACACCCCAAGTACTCTCTCCGAGGCTTGACCCC 875
809 A-----GCTCAACTTCAGGACAGCCACTCACTGTGGGAGCA 847
876 AAGCAGTGCCTGCTCGCTCAGCTTACACTTCAGTTTGCA---AATACACAGATC 932
848 CCGGTGTGGAGGCCGACCTGCTCAAGCTCTATGAATCCGCTTGCACATCTCTGTC 907
933 AATGGCACCACCGCAGCTCATCAAGGCTTACGGGATCCGCAATTCAGCTCAATGTG 992
908 ACCGGCAGCAGGAGGAGTGGGCTCATCCCGACCGGCTGCACACTGGGACCGGGCA 967
993 CATGGACAGCGCGGAGTTACGCTGATCCACCATTAATTAATCTGGCCACAGCTGTG 1052
968 GCTTGGCTGGGCTGCTACCTTTTCTGTGACCTGCTACTGCTGTATGTGGATAGAAA 1027
1053 ACTTCGCTGGGTGGGCTCTCTGTCGAGTGTGATCTTGTCTTAACATTCATGAACAA 1112
1028 GCCCATTTCTAGGAGGACAAAGTATGAGGAGGCGCAAGGCCCGCA 1073
1113 AACAGGCTCTACAGCCATAAGAAATTTGACAAAGTGTGTACGCCGA 1158

RESULT 14
US-09-191-608-13
; Sequence 13, Application US/09191608
; Patent No. 6242216
; GENERAL INFORMATION:
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Metzger, Randy E.
; APPLICANT: Niforatos, Wende
; APPLICANT: Touma, Edward B.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding a Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of Production
; TITLE OF INVENTION: And Use Thereof
; FILE REFERENCE: 6394 US P1
; CURRENT APPLICATION NUMBER: US/09/191,608
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-191-608-13

Query Match 7.9%; Score 213.2; DB 3; Length 1436;
Best Local Similarity 55.0%; Pred. No. 7,8e-45;
Matches 553; Conservative 0; Mismatches 408; Indels 45; Gaps 5;

QY 92 GAGAAGTGGCTCTCTCCGCAAAAAGGCTACCCAGGAGCGGACCTGGAAACCCAGTTT 151
Db 174 GTGTGTGATGATTCATCTGTGAGAAAAGTACAGGAGAGGAGACGGGCCCGAGAGC 233
QY 152 TCCATCATCACCAAACTCAAAAGGGTTCCTGTCATCTCAGATCAAGAGCTTGGAAACCG 211
Db 234 TCCATCATCACCAAGTCAAGGGATCACCACTCCGAGCACAAA----- 279
QY 212 CTGTGGATGTGGCGACTTCGTGAAAGCCACTCAGGAGAGAACGTGTCTCTTTGGTG 271
Db 280 -TGTGGAGCTGTGGAGGATACGTGAAGCCCCCGAGGGGGGAGCGTGTTCAGCATCATC 338
QY 272 ACCAACTTCTGTGAGCGCCAGCCCAAGTTTCAGGCGAGATGCCAGAGCACCCGTCGTC 331
Db 339 ACCAGGTTCAGGCGCACCTCCAGACCCAGGAACTGCCCCGAGAGCATAAGGGTC 398
QY 332 CCACTGCTTAACCTGCTGGTTCAGAGGACTGCCCCAAGGGAGGAGGACACACAGC 391
Db 399 CACAACGCCACTCTCTCCGACGCCGACTGCGTGGCTGGGAGCTGGACATGCTGGGA 458
QY 392 CAGGTGTAAACACAGCCAGTGTGTG---GTGTTCAATGGGACCCACAGAGCTGTGAG 448
Db 459 AAGCGCTGAGGACCGGGCGCTGTGTGCCCTATTACAGGGGCTCTCCAGAGACTGGAG 518
QY 449 ATCTGGAGTTGGTCCAGTGGAGAGTGGCTGTGTGCCCTCGAGGCGCTCTGTGGCCAG 508
Db 519 GTGTTCGGCTGTGTCGGTGGAGATGGGCGCTCTGTACAGCAATTTCTGGGTACGATG 578
QY 509 GCCCAGAACTTCACTGTTCATCAAAAACACAGTCACTTTCAGGAGTTCAATCTCT 568
Db 579 GCCCAGAAATTTCACTTCACTCAAGACAGCATCCACTTACCCCAATTTCCATCTCTCC 638
QY 569 AAGTCCAAATGCTTGGAGACTGGGACCCCACTATTTTAAAGCATGCGGTATGAACCA 628
Db 639 AAGGGCAACATCGCCGACCGCACAGA---CGGGTACCTGAAGCGCTGCACGTTCCACGAG 695
QY 629 CAATTCAGCCCTACTGTCCTGTTCGCGATTTGGGACCTCGTGCCCAAGGCTGGAGGG 688
Db 696 GCTTCGACCTTACTGCCCCATCTTCAAGCTGGGCTTTATCGTGGAGAGCTGGGGAG 755
QY 689 ACCTTCGAGGACCTGGCGTTGCTGGGTGGCTCTGTAGGCATCAGAGTTCACTGGGAATGT 748
Db 756 ACCTTCAGAGCTCGCACACAGGGTGTGTGTCATCGGGTCAATTAACAGTGGACTGT 815
QY 749 GACCTGGACACCGGGGACTGTGGCTGTGGCTCTACTACTCTTCCASCTGCAGAGAG 808
Db 816 GACCTGGACCTCGCATCGAGTGCACACCCCAAGTACTCTCTCCGAGGCTTGACCCC 875
QY 809 A-----GCTCAACTTCAGGACAGCCACTCACTGTGGGAGCA 847
Db 876 AAGCAGTGCCTGCTCGCTCAGCTTACACTTCAGTTTGCA---AATACACAGATC 932
QY 848 CCGGTGTGGAGGCCGACCTGCTCAAGCTCTATGAATCCGCTTGCACATCTCTGTC 907
Db 933 AATGGCACCACCGCAGCTCATCAAGGCTTACGGGATCCGCAATTCAGCTCAATGTG 992
QY 908 ACCGGCAGCAGGAGGAGTGGGCTCATCCCGACCGGCTGCACACTGGGACCGGGCA 967
Db 993 CATGGACAGCGCGGAGTTACGCTGATCCACCATTAATTAATCTGGCCACAGCTGTG 1052
QY 968 GCTTGGCTGGGCTGCTACCTTTTCTGTGACCTGCTACTGCTGTATGTGGATAGAAA 1027
Db 1113 AACAGGCTCTACAGCCATAAGAAATTTGACAAAGTGTGTACGCCGA 1158

Db 1053 ACTTCGTCGGGTGGGCTCCTTCGTGCGACTGGATCTTCTAATCATGACAAA 1112

Qy 1028 GCCATTTCTACTGGAGGCAAAAGTATAGGAGGCCAAGGCCCGA 1073

Db 1113 AACAGGTCTACAGCCATAAGAAATTTGACAAGGTGTGTACGCCGA 1158

RESULT 15

US-08-750-134A-4

; Sequence 4, Application US/08750134A

; Patent No. 5985603

; GENERAL INFORMATION:

; APPLICANT: VALERA, SOLEDAD

; APPLICANT: BUELL, GARY

; TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/750,134A

; FILING DATE: 22-JAN-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: CRAWFORD, ARTHUR C.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 1430-116

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4006

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1837 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; CLONE: rat P2x from vas deferens

US-08-750-134A-4

Query Match 7.6%; Score 206; DB 2; Length 1837;

Best Local Similarity 54.1%; Pred. No. 6.3e-43;

Matches 500; Conservative 0; Mismatches 400; Indels 24; Gaps 3;

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Db 411 AAGCTCAAGGGCTTGGTGTGTGACCCAGCTCCAGGGCTGGGACCCAGGCTGGGACGTG 470

Qy 224 GCCGACTTCGTGAAGCCACCTCAGGAGGAGAAAGTGTCTTCTTGGTGACCAACTTCCTT 283

Db 471 GCTGACTATGTCTTCCAGGACACAGGGGACAGCTCCTTTGTAGTTATGACCAACTTCATC 530

Qy 284 GTGACGCCAGCCCAAGTTCAAGGAGAGATGCCAGAGCACCGCTCCGCTCCACTGGCTAAC 343

Db 531 GTGACCCCTCAGCAGACTCAAGGCCATTGTGACAGAAACCC-----AGAAGGTGCATA 584

Qy 344 TGCTGGGTGACAGGAGTCTCCCGAGGGGAGGGAGGACACACAGCCACCGGTGTAAAAA 403

Db 585 TGCCAGGATGACAGTGGCTGCTCACTCCAGGAAAGAGCAGAAAGAAAGCCCAAGGTATTCGC 644

Qy 404 ACAGGCCAGTGTGGTGTCTCAATGGGACCCACAGGACCTGTGAGATCTGGAGTTGGTGC 463

Db 645 ACAGGCAACTGTGTGCCCTTCAATGGCACTGTGAAGACATGTGAGATCTTTGGTTGGTGT 704

Search completed: November 21, 2004, 17:43:04

Job time : 230.653 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 12:30:45 ; Search time 1290.69 Seconds
(without alignments)
10552.804 Million cell updates/sec

Title: US-09-820-095B-1
Perfect score: 2693
Sequence: 1 ttgtgactatgcccgc.....aaaaaaaaaaaaaaaaaaaaa 2693

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1592.6	59.1	16449	8 AAL51049	Aal51049 Human P2X
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5	1174	43.6	1452	12 ADP49172	Adp49172 Human P2X
6	1174	43.6	1452	12 ADP49182	Adp49182 Human P2X
7	1174	43.6	1452	12 ADP49174	Adp49174 Rat P2X2
8	1174	43.6	1452	12 ADP49176	Adp49176 Human P2X
9	1162.4	43.2	1360	4 AAD04978	Aad04978 Human pur
10	1155.8	42.9	1293	2 AAV61832	Aav61832 Coding se
11	678.4	25.2	800	12 ADP28208	Adp28208 Human sec
12	567.4	21.1	569	4 AAL18520	Aal18520 Probe #84
13	567.4	21.1	569	4 ABA63528	Aba63528 Human foe
14	567.4	21.1	569	4 AAI43639	Aai43639 Probe #12
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16	567.4	21.1	569	4 AAK37767	Aak37767 Human bon
17	567.4	21.1	569	4 AAK12055	Aak12055 Human bra
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ALIGNMENTS

RESULT 1

AAAL51048	AAAL51048 standard; cDNA; 2693 BP.
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XX	AAAL51048;
DT	20-FEB-2003 (first entry)
DE	Human P2X-like purinergic receptor G-protein coupled receptor cDNA.
XX	Human; gene; ss; gene therapy; G-protein coupled receptor; chromosome 22;
KW	P2X-like purinergic receptor; anaplastic oligodendroglioma; GPCR;
KW	chronic lymphocytic leukaemia; lung carcinoma; colon carcinoma;
KW	brain carcinoma; drug screening; tissue typing; pharmacogenomic analysis;
KW	single nucleotide polymorphism; SNP.
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FT	WO200279229-A2.
FT	10-OCT-2002.
FT	28-MAR-2002; 2002WO-US009545.
FT	29-MAR-2001; 2001US-00820095.
FT	(PEKE) PE CORP NY.
FT	Wei M, Gong F, Di Francesco V, Beasley EM;
FT	WPI; 2003-040648/03.
FT	P-PSDB; AAO15997.
FT	New peptides related to P2X-like purinergic receptor subfamily, useful for

PT treating disorders associated with abnormal expression of protease in
 PT anaplastic oligodendroglioma, leukemia, carcinoid lung, or large cell
 PT lung carcinoma.

XX Claim 4; Fig 1A; 87pp; English.

XX The invention comprises the amino acid and coding sequence (located on
 CC chromosome 22) of a human G-protein coupled receptor (GPCR) which is
 CC related to the P2X-like purinergic receptor subfamily. The DNA and
 CC protein sequences of the invention are useful for treating: anaplastic
 CC oligodendroglioma; chronic lymphocytic leukemia; lung carcinoma; colon
 CC carcinoma; and brain carcinoma. The DNA and protein sequences of the
 CC invention are also useful for drug screening assays, tissue typing and
 CC pharmacogenomic analysis. The present cDNA sequence encodes the human
 CC GPCR that is related to the P2X-like purinergic receptor subfamily

XX Sequence 2693 BP; 579 A; 761 C; 821 G; 532 T; 0 U; 0 Other;

Query Match 100.0%; Score 2693; DB 8; Length 2693;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	GACAGGCTGGGGGCTTCTGGATTATAGACGAGAGTGGGCTCTCTCGCCAAAAGG	120
QY	121	CTACAGAGCGGAGCTGGAAACCCAGTTTTCATCATCAACCACTCAAGGGTTTC	180
DB	121	CTACAGAGCGGAGCTGGAAACCCAGTTTTCATCATCAACCACTCAAGGGTTTC	180
QY	181	CGTCACTCAGATCAAGGAGCTGGAAACCCAGTTTTCATCATCAACCACTCAAGGGTTTC	240
DB	181	CGTCACTCAGATCAAGGAGCTGGAAACCCAGTTTTCATCATCAACCACTCAAGGGTTTC	240
QY	241	ACCTCAGGAGAGAACGTTTCTTCTTGGTGACCACTTCTTGACGCCAGCCCAAGT	300
DB	241	ACCTCAGGAGAGAACGTTTCTTCTTGGTGACCACTTCTTGACGCCAGCCCAAGT	300
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QY	361	CTGCCCCGAGGGGAGGAGCACAACAGCCGCTGTAACAAACAGGCCAGTGTGGT	420
DB	361	CTGCCCCGAGGGGAGGAGCACAACAGCCGCTGTAACAAACAGGCCAGTGTGGT	420
QY	421	GTTCAATGGGACCAACAGGACCTGTGAGATCTGGAGTTGTGTCAGTGGAGTGGCGT	480
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DB	541	AGTCACTTCAGAGCCCTGTGTCGCCAGGCCAGACTTCACACTGTTTCAATCAAAACAC	600
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RESULT 2
ID AAL51049
XX AAL51049 standard; DNA; 16449 BP.
AC AAL51049;
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DT 20-FEB-2003 (first entry)
DE Human P2X-like purinergic receptor G-protein coupled receptor gene.
XX
KW Human; gene; ds; gene therapy; G-protein coupled receptor; chromosome 22;
KW P2X-like purinergic receptor; anaplastic oligodendroglioma; GPCR;
KW chronic lymphocytic leukaemia; lung carcinoma; colon carcinoma;
KW brain carcinoma; drug screening; tissue typing; pharmacogenomic analysis;
XX SNP; single nucleotide polymorphism.
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 PI Wei M, Gong F, Di Francesco V, Beasley EM;
 XX WPI; 2003-040648/03.
 DR P-PSDB; AAO15997.
 XX
 PT New peptides related to P2X-like purigenic receptor subfamily, useful for
 PT treating disorders associated with abnormal expression of protease in
 PT anaplastic oligodendroglioma, leukemia, carcinoid lung, or large cell
 PT lung carcinoma.
 XX
 PS Claim 4; Fig 3A-E; 87pp; English.
 XX
 CC The invention comprises the amino acid and coding sequence (located on
 CC chromosome 22) of a human G-protein coupled receptor (GPCR) which is
 CC related to the P2X-like purigenic receptor subfamily. The DNA and
 CC protein sequences of the invention are useful for treating: anaplastic
 CC oligodendroglioma; chronic lymphocytic leukaemia; lung carcinoma; colon
 CC carcinoma; and brain carcinoma. The DNA and protein sequences of the
 CC invention are also useful for drug screening assays, tissue typing and
 CC pharmacogenomic analysis. The present genomic DNA sequence represents the
 CC gene encoding the human GPCR that is related to the P2X-like purigenic
 CC receptor subfamily
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 Best Local Similarity 99.7%; Pred. No. 0;
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 QY 2073 TTCTGAGAGCCCTGGGGGTGGAGGCTGTGGAGGCTGTACCTGAAATTCATTGAG 2132
 DB 14266 TTCTGAGAGCCCTGGGGGTGGAGGCTGTGGAGGCTGTACCTGAAATTCATTGAG 14325
 QY 2133 TCCAACTCATCTAGGAAGCTGTCTGGGACGCTGCTGAGGAGGCGCTGCTGATC 2192
 DB 14326 TCCAACTCATCTAGGAAGCTGTCTGGGACGCTGCTGAGGAGGCGCTGCTGATC 14385
 QY 2193 CCAGGCTGATGGAGTGGTGAAGAAATGTTCCAAACACACACGAGATCTCCCTC 2252
 DB 14386 CCAGGCTGATGGAGTGGTGAAGAAATGTTCCAAACACACACGAGATCTCCCTC 14445
 QY 2253 AGGCTGGCCAGCTTTTGAGCTGGAATCTCTCTGTGCTCCAGGCGGGGAGGAAT 2312
 DB 14446 AGGCTGGCCAGCTTTTGAGCTGGAATCTCTCTGTGCTCCAGGCGGGGAGGAAT 14505
 QY 2313 CTAAGTGTCCACCCAGGAGGCAAGGGGCTGCTTCCACTGTGGGTACCTGGTGATCAG 2372
 DB 14506 CTAAGTGTCCACCCAGGAGGCAAGGGGCTGCTTCCACTGTGGGTACCTGGTGATCAG 14565
 QY 2373 GGCAGCTGTGAGGCGCCAGGGGTGGGCTGAGACTGGGCTGACATCTAGAAATCACCTGC 2432
 DB 14566 GGCAGCTGTGAGGCGCCAGGGGTGGGCTGAGACTGGGCTGACATCTAGAAATCACCTGC 14625
 QY 2433 CACCTGGAGCCTCAGTAAATGCTTGGGTCCCTGCTGCTCAATCTCCAGAGCCATG 2492
 DB 14626 CACCTGGAGCCTCAGTAAATGCTTGGGTCCCTGCTGCTCAATCTCCAGAGCCATG 14685
 QY 2493 TCCTATGGGAGTGGGCTCTGAAGGGCGAAAGTGGAGAGAGGCGCCCTCAGGCTGGG 2552
 DB 14686 TCCTATGGGAGTGGGCTCTGAAGGGCGAAAGTGGAGAGAGGCGCCCTCAGGCTGGG 14745
 QY 2553 TATCCAAGGAGGCGACGTGACCTGATTCCTCTTGGGCGCCAGAGGAGCTGATCAT 2612
 DB 14746 TATCCAAGGAGGCGACGTGACCTGATTCCTCTTGGGCGCCAGAGGAGCTGATCAT 14805
 QY 2613 GGCTGGACAAAGTCAAGGAGTAAAGCCAGCAAGCCACC 2651
 DB 14806 GGCTGGACAAAGTCAAGGAGTAAAGCCAGCAAGCCACC 14844

RESULT 3

AAV61833

ID AAV61833 standard; cDNA; 1697 BP.

XX

XX AAV61833;

XX

DT 28-APR-1999 (first entry)

XX Coding sequence for human p53 regulated protein, P2XM.
 DE
 XX
 KW Human; p53 regulated protein; P2XM; ATP receptor; RP-2 protein;
 KW thymocyte; apoptosis; tumour-suppressor gene; rhabdoid sarcoma;
 KW anticancer drug; ss.
 XX
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT CDS 46..1341
 FT /*tag= a

XX WO9842835-A1.

XX 01-OCT-1998.

XX 18-MAR-1998; 98WO-JP001146.

XX 26-MAR-1997; 97JP-00093044.

XX (SAKA) OTSUKA PHARM CO LTD.

XX Tokino T, Nakamura Y;

XX WPI; 1998-532006/45.

XX P-PSDB; AAW76434.

Human gene P2XM whose transcription is induced by p53 - useful, e.g. for
 diagnostic purposes and in development of new anticancer drugs.

XX Disclosure; Page 23-27; 43pp; Japanese.

This sequence represents the coding sequence for the P2XM protein of the
 invention. The protein is significantly homologous to: (i) the P2X family
 of ATP receptors, and (ii) RP-2 protein which is expressed in thymocytes
 during apoptosis. Transcription of the genes is specifically regulated by
 the tumour-suppressor gene p53. The P2XM gene is specifically expressed
 in skeletal muscle and has been localised to chromosome 22q11, an area
 where mutation and sequence losses frequently occur in rhabdoid sarcomas.
 The genes may be used for diagnostic purposes (e.g. by detecting changes
 occurring in the gene in sarcomas), using probes and primers containing
 or derived from all or part of the genes. The genes may further be used
 in the development of new anticancer drugs

XX SQ Sequence 1697 BP; 343 A; 496 C; 520 G; 338 T; 0 U; 0 Other;

Query Match 56.2%; Score 1513.8; DB 2; Length 1697;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1511; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 97 GTGGGCTCTCTCGCCAAAAGGCTACCGAGGCGGACCTGGAAACCCAGTTTCCAT 156
 DB 180 GTGGGCGCTCTCGCCAAAAGGCTACCGAGGCGGACCTGGAAACCCAGTTTCCAT 239
 QY 157 CATCACCAACTCAAGGGGTTTCCCTCACTCAGATCAAGGAGCTTGGAAACCGGCTGTG 216
 DB 240 CATCACCAACTCAAGGGGTTTCCCTCACTCAGATCAAGGAGCTTGGAAACCGGCTGTG 299
 QY 217 GGATGTGGCGGACTTCGTGAAGCCACTCAGGAGAGAAACGTGTTCTTCTTGTGACCAA 276
 DB 300 GGATGTGGCGGACTTCGTGAAGCCACTCAGGAGAGAAACGTGTTCTTCTTGTGACCAA 359
 QY 277 CTTTCTTGTGACGCCAGCCCAAGTTTCAGGGCAGATGCCAGAGCACCCGCTCCACT 336
 DB 360 CTTTCTTGTGACGCCAGCCCAAGTTTCAGGGCAGATGCCAGAGCACCCGCTCCACT 419
 QY 337 GGCTAACTGTGGGTGCGAGGACTGCCCCGAAGGGAGGGAGGCACACAGCCACCG 396
 DB 420 GGCTAACTGTGGGTGCGAGGACTGCCCCGAAGGGAGGGAGGCACACAGCCACCG 479
 QY 397 TGTAAAAACAGGCCAGCTGTGTGTGTTCAATGGGACCCACAGGACCTGTGAGATCTGGAG 456

Db 480 TGTAAAAACAGCCAGTGTGTGGTTCAATGGGACCCACAGGACCTGTGAGATCTGGAG 539
Qy 457 TTGTTGCCAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGTCGCCAGGCCAGAA 516
Db 540 TTGTTGCCCTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGTCGCCAGGCCAGAA 599
Qy 517 CTTACACTGTTATCAAAAACAGTCACTTTCAGCAAGTTCAACTTCTTAAGTCCAA 576
Db 600 CTTACACTGTTATCAAAAACAGTCACTTTCAGCAAGTTCAACTTCTTAAGTCCAA 659
Qy 577 TGCCTTGAGACCTGGGACCCCACTATTTAAGCACTGCGCTATGAACCAAAATTCAG 636
Db 660 TGCCTTGAGACCTGGGACCCCACTATTTAAGCACTGCGCTATGAACCAAAATTCAG 719
Qy 637 CCCCTACTGTCCGTTGTTCCGATTTGGGACCTCGTGGCCAAAGCTGGAGGACCTTCGA 696
Db 720 CCCCTACTGTCCGTTGTTCCGATTTGGGACCTCGTGGCCAAAGCTGGAGGACCTTCGA 779
Qy 697 GGAAGTGGCTGTGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATTTGTGACCTGGA 756
Db 780 GGAAGTGGCTGTGGTGGCTCTGTAGGCATCAGAGTTCACTGGGATTTGTGACCTGGA 839
Qy 757 CACCGGGACCTGTGGCTGTGGCTCTACTCTTCCAGTGCAGGAGAGAGTCAAA 816
Db 840 CACCGGGACCTGTGGCTGTGGCTCTACTCTTCCAGTGCAGGAGAGAGTCAAA 899
Qy 817 CTTAGGACAGCACTCACTGGTGGGACCAACCGGTTGGAGGCCCGCACCTGCTCAA 876
Db 900 CTTAGGACAGCACTCACTGGTGGGACCAACCGGTTGGAGGCCCGCACCTGCTCAA 959
Qy 877 GCTCTATGAAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGAGTTGCGGCTCAT 936
Db 960 GCTCTATGAAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGAGTTGCGGCTCAT 1019
Qy 937 CCCACGGCGCTCACTGGGACCGGGGAGCTTGGCTGGGCTGTGTCACCTTTTCTG 996
Db 1020 CCCACGGCGCTCACTGGGACCGGGGAGCTTGGCTGGGCTGTGTCACCTTTTCTG 1079
Qy 997 TGACCTGTCTGTGTATGTAGTAAAGACCCATTTCTACTGGAGGACAAAGTATGA 1056
Db 1080 TGACCTGTCTGTGTATGTAGTAAAGACCCATTTCTACTGGAGGACAAAGTATGA 1139
Qy 1057 GGAGGCCAAGCCCGAACCAACCGCAACTCTGTGTGGAGGAGCTGGCCCTTGATC 1116
Db 1140 GGAGGCCAAGCCCGAACCAACCGCAACTCTGTGTGGAGGAGCTGGCCCTTGATC 1199
Qy 1117 CCAGCCCGAGTGGCGGAGTGCCTCAGACGGAGCTCAGCCTGCACCCAGGCCACTGC 1176
Db 1200 CCAGCCCGAGTGGCGGAGTGCCTCAGACGGAGCTCAGCCTGCACCCAGGCCACTGC 1259
Qy 1177 TGCTGGGAGTCAACACAGACACCAAGTGGCCCTGTCCAAAGTTCTGACACCCACTGGC 1236
Db 1260 TGCTGGGAGTCAACACAGACACCAAGTGGCCCTGTCCAAAGTTCTGACACCCACTGGC 1319
Qy 1237 AACCAATTCGGGACCTGTAGCCCTTCCCTGCTGGTTGAGAGTTGGGGCTGGGAGG 1296
Db 1320 AACCAATTCGGGACCTGTAGCCCTTCCCTGCTGGTTGAGAGTTGGGGCTGGGAGG 1379
Qy 1297 CGGGCCCTGCTGGGGATCTCAAGGATGAGGCCCCAGCAGTGGAGGATTTGGGGTAGAAT 1356
Db 1380 CGGGCCCTGCTGGGGATTTCAAGGATGAGGCCCCAGCAGTGGAGGATTTGGGGTAGAAT 1439
Qy 1357 TCCACCTTGAACCCAGACAGATGCCCTCCCTGTGATCCCACTTGTGAGGTTGCTGC 1416
Db 1440 TCCACCTTGAACCCAGACAGATGCCCTCCCTGTGATCCCACTTGTGAGGTTGCTGC 1499
Qy 1417 CTCAGGAGCCATAGAAGTGGCTGTGTTTGAACGGCGACAGAACTGACCCCTGGAG 1476
Db 1500 CTCAGGAGCCATAGAAGTGGCTGTGTTTGAACGGCGACAGAACTGACCCCTGGAG 1559
Qy 1477 ACTGGAGAGCCAGCAGGACCTGTATGTGAGGCTCCGACTGTGTCAGGGGCTC 1536
Db 1560 ACTGGAGAGCCAGCAGGACCTGTATGTGAGGCTCCGACTGTGATGTGGAGGGCTC 1619

Qy 1537 CTGCTGGCTCTGGGCTGGAGGTCTCTCTCCAGTGTCTCTGCCAGTGTCTCTAGCAG 1596
Db 1620 CTGCTGGCTCTGGGCTGGAGGTCTCTCTCCAGTGTCTCTGCCAGTGTCTCTAGCAG 1679
Qy 1597 AGGTATGCTTACCAGCTG 1614
Db 1680 AGGTATGCTTACCAGCTG 1697
RESULT 4
ADP49178
ID ADP49178 standard; DNA; 1452 BP.
XX
AC ADP49178;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human P2X4 purinergic receptor DNA sequence for odour modulation.
XX
ds; gene; odour sensitivity; P2X purinergic receptor;
KW P2Y purinergic receptor; signal transduction pathway;
KW Olfactory signalling; micro-array.
XX
OS Homo sapiens.
XX WO2004047749-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037389.
XX
PR 21-NOV-2002; 2002US-0428140P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Lucero M, Hegg C;
XX
XX WPI; 2004-460642/43.
XX
DR Modulating odor sensitivity in a subject, comprises administering a
PT composition comprising an agonist or antagonist of P2X or P2Y purinergic
PT receptor to the subject.
XX
PS Disclosure; SEQ ID NO 7; 108pp; English.
XX
CC The invention relates to a method of modulating (M1) odour sensitivity in
CC a subject, by administering a composition which is an agonist or
CC antagonist of a P2X or P2Y purinergic receptor. (M1) is useful for
CC modulating odour sensitivity in a subject (claimed). The compositions
CC used for modulating odour sensitivity in a subject are useful for
CC studying the signal transduction pathways related to olfactory signaling.
CC The compositions are also useful as reagents in micro-arrays or as
CC reagents to probe or analyze existing micro-arrays. This sequence
CC corresponds to the human P2X4 DNA sequence.
XX
XX Sequence 1452 BP; 316 A; 415 C; 442 G; 279 T; 0 U; 0 Other;
SQ

Query Match 43.6%; Score 1174; DB 12; Length 1452;
Best Local Similarity 97.2%; Pred. No. 3.2e-267;
Matches 1219; Conservative 0; Mismatches 25; Indels 10; Gaps 2;
Qy 97 GTGGGCTCTCTCGCCAAAAGGCTTACCAGAGCGGACCTGGAAACCCAGTTTCCAT 156
Db 179 GTGGGCTCTCTCGCCAAAAGGCTTACCAGAGCGGACCTGGAAACCCAGTTTCCAT 238
Qy 157 CATCACAAACTCAAGGGTTTCCGTCATCAGATCAAGGAGCTTGAACCCGCTGTG 216
Db 239 CATCACAAACTCAAGGGTTTCCGTCATCAGATCAAGGAGCTTGAACCCGCTGTG 298
Qy 217 GGAATGGCCGACTTCGTGAAGCCACCTCAGGAGAGACGTGTTCTTCTTGGTACCAA 276
Db 299 GGAATGGCCGACTTCGTGAAGCCACCTCAGGAGAGACGTGTTCTTCTTGGTACCAA 358

QY 277 CTTCTCTGTGAGCCAGCCAAAGTTTCAGGCGAGATGCCCAGAGCACCCGTCGTCCTCCACT 336
Db 359 CTTCTCTGTGAGCCAGCCAAAGTTTCAGGCGAGATGCCCAGAGCACCCGTCGTCCTCCACT 418
QY 337 GGTCTAACTCTGGTTCGAGAGACTGCCCCGAGGGAGGAGGACACACAGCCACGG 396
Db 419 GGTCTAACTCTGGTTCGAGAGACTGCCCCGAGGGAGGAGGACACACAGCCACGG 478
QY 397 TGTAAAAACAGGCCAGTGTGTGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGAG 456
Db 479 TGTAAAAACAGGCCAGTGTGTGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGAG 538
QY 457 TTGGTCCCAAGTGGAGAGTGGTGTGTGCTCCCTGAGGCCCTCTGGGCCAGGCCAGAA 516
Db 539 TTGGTCCCAAGTGGAGAGTGGTGTGTGCTCCCTGAGGCCCTCTGGGCCAGGCCAGAA 598
QY 517 CTTACACACTGTTTCATCAAAAAACACAGTCACTCTTCAGCAAGTTCAACTTCTCTAAGTCCAA 576
Db 599 CTTACACACTGTTTCATCAAAAAACACAGTCACTCTTCAGCAAGTTCAACTTCTCTAAGTCCAA 658
QY 577 TGGCTTGGAGACTGGGACCCACCTATTTTAAGCACTGCCGCTATGAACCAATTCAG 636
Db 659 TGGCTTGGAGACTGGGACCCACCTATTTTAAGCACTGCCGCTATGAACCAATTCAG 718
QY 637 CCGCTACTGTCCGCTGTTCCGCAATGGGCACTCTGTCGCAAGGCTGGAGGACCTTCGA 696
Db 719 CCGCTACTGTCCGCTGTTCCGCAATGGGCACTCTGTCGCAAGGCTGGAGGACCTTCGA 778
QY 697 GGAACCTGGCGTCTGCTGGTGTCTGTAGGCATCAAGTTCACTGGATTTGACCTCGA 756
Db 779 GGAACCTGGCGTCTGCTGGTGTCTGTAGGCATCAAGTTCACTGGATTTGACCTCGA 838
QY 757 CACCGGGACTCTGGCTGCTGGCTCACTACTCTTCAGCTGCAAGGAGAGAGTACAA 816
Db 839 CACCGGGACTCTGGCTGCTGGCTCACTACTCTTCAGCTGCAAGGAGAGAGTACAA 898
QY 817 CTTACGAGCAGCACTCACTGTGGGAGCAACCGGCTGTGGAGGCCGACCCCTCTCAA 876
Db 899 CTTACGAGCAGCACTCACTGTGGGAGCAACCGGCTGTGGAGGCCGACCCCTCTCAA 958
QY 877 GCTCTATGAATCCGCTTGCATCTGTCTACCGGCGAGGAGAGTTCGGCTCAT 936
Db 959 GCTCTATGAATCCGCTTGCATCTGTCTACCGGCGAGGAGAGTTCGGCTCAT 1018
QY 937 CCCCAGCGCGTCACTGGGACACCGGGCAGCTTGGCTGGCGTGGTCACTTTTCTG 996
Db 1019 CCCCAGCGCGTCACTGGGACACCGGGCAGCTTGGCTGGCGTGGTCACTTTTCTG 1078
QY 997 TGACCTGTCTACTGTGTATGTGATAGAGAACCCATTTCTACTGGAGACAAAGTATGA 1056
Db 1079 TGACCTGTCTACTGTGTATGTGATAGAGAACCCATTTCTACTGGAGACAAAGTATGA 1138
QY 1057 GGAGGSCAAGGCCCGGAAAGCAACCGCAACTCTGTGTGGAGGAGCTGGCCCTTGCAATC 1116
Db 1139 GGAGGSCAAGGCCCGGAAAGCAACCGCCAACTCTGTGTGGAGGAGCTGGCCCTTGCAATC 1198
QY 1117 CCAAGCCGACTGGCCGAGTGCCTCAGACGGAGCTCAGCACTGCAACCCAGCCGCACTGC 1176
Db 1199 CCAAGCCGACTGGCCGAGTGCCTCAGACGGAGCTCAGCACTGCAACCCAGCCGCACTGC 1258
QY 1177 TGCTGGAGTCAACACAGACACCCAGGATGGCCCTGTCCAAGTTCTGACACCCACTTGC 1236
Db 1259 TGCTGGAGTCAACACAGACACCCAGGATGGCCCTGTCCAAGTTCTGACACCCACTTGC 1318
QY 1237 AACCCATTCCGGAGGCTGTAGCCG-TTCCCTGTCTGGTTGAGA-----GTTGGGGG 1286
Db 1319 AACCCATTCCGGAGGCTGTAGCCGTTTCCCTGTCTGGTTGAGAAGAGAGGGGCTGGGC 1378
QY 1287 CTGGGAAGGGGGGCGCTCTGCTGGGATCTCAAGATAGAGCCCCAGATGGA 1340
Db 1379 AAGGAAGGAGCCCTGCTGCTGCGAGCGAAAGCAAGGATGAGGCAACAGCAATGA 1432

RESULT 5
ADP49172
ID ADP49172 standard; DNA; 1452 BP.
XX
AC ADP49172;
XX
DT 26-AUG-2004 (first entry)
XX
Human P2X1 purinergic receptor DNA sequence for odour modulation.
DE ds; gene; odour sensitivity; P2X purinergic receptor;
XX P2Y purinergic receptor; signal transduction pathway;
KW olfactory signalling; micro-array.
XX
OS Homo sapiens.
XX
PN WO2004047749-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037389.
XX
PR 21-NOV-2002; 2002US-0428140P.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Lucero M, Hegg C;
XX
DR WPI; 2004-460642/43.
XX
Modulating odor sensitivity in a subject, comprises administering a
PT composition comprising an agonist or antagonist of P2X or P2Y purinergic
PT receptor to the subject.
XX
PS Disclosure; SEQ ID NO 1; 108pp; English.
XX
The invention relates to a method of modulating (M1) odour sensitivity in
CC a subject, by administering a composition which is an agonist or
CC antagonist of a P2X or P2Y purinergic receptor. (M1) is useful for
CC modulating odour sensitivity in a subject (claimed). The compositions
CC used for modulating odour sensitivity in a subject are useful for
CC studying the signal transduction pathways related to olfactory signaling.
CC The compositions are also useful as reagents in micro-arrays or as
CC reagents to probe or analyze existing micro-arrays. This sequence
CC corresponds to the human P2X1 DNA sequence.
XX
SQ Sequence 1452 BP; 316 A; 415 C; 442 G; 279 T; 0 U; 0 Other;

Query Match 43.6%; Score 1174; DB 12; Length 1452;
Best Local Similarity 97.2%; Pred. No. 3.2e-267;
Matches 1219; Conservative 0; Mismatches 25; Indels 10; Gaps 2;
QY 97 GTGGGCTCTCTCGCCAAAAGAGCTACAGGAGCGGACCTGGAACCCCGATTTTCCAT 156
Db 179 GTGGGCTCTCTCGCCAAAAGAGCTACAGGAGCGGACCTGGAACCCCGATTTTCCAT 238
QY 157 CATCAACAAACTCAAAGGGGTTTCCGTCACTCAGATCAAGGAGCTTGGAAACCGGCTGTG 216
Db 239 CATCAACAAACTCAAAGGGGTTTCCGTCACTCAGATCAAGGAGCTTGGAAACCGGCTGTG 298
QY 217 GGATGTGGCGACTTGTGTAAGCCACTCAGGAGAGAGAGTGTCTTCTTGTGTGACCA 276
Db 299 GGATGTGGCGACTTGTGTAAGCCACTCAGGAGAGAGAGTGTCTTCTTGTGTGACCA 358
QY 277 CTTCTTGTGACGCCACCCCAAGTTTCAGGGCAGATGCCAGAGACCCCGTCCGCTCCACT 336
Db 359 CTTCTTGTGACGCCACCCCAAGTTTCAGGGCAGATGCCAGAGACCCCGTCCGCTCCACT 418
QY 337 GGCTAACTGTGGTTCGAGGAGTGTCCCGAAGGGAGGAGGACACACAGACCAACGG 396
Db 419 GGCTAACTGTGGTTCGAGGAGTGTCCCGAAGGGAGGAGGACACACAGACCAACGG 478

QY 397 TGTAAAAACAGCCAGTGTGTGGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGGAG 456
DB 479 TGTAAAAACAGCCAGTGTGTGGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGGAG 538
QY 457 TTGGTGCCCAAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGCGCCAGGCGCCAGAA 516
DB 539 TTGGTGCCCAAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGCGCCAGGCGCCAGAA 598
QY 517 CTTACACATGTTCATCAAAAAACAGATCACCTTCCAGCAAGTTCACATCTCTTAAGTCCAA 576
DB 599 CTTACACATGTTCATCAAAAAACAGATCACCTTCCAGCAAGTTCACATCTCTTAAGTCCAA 658
QY 577 TGCCTTGGAGACCTGGGACCCCACTATTTAAGCACTGCGCTATGAACCAACAATTGAG 636
DB 659 TGCCTTGGAGACCTGGGACCCCACTATTTAAGCACTGCGCTATGAACCAACAATTGAG 718
QY 637 CCCCTACTGTCCCGTGTTCGCAATGGGACCTCGTGCCCAAGCTGGAGGGACCTTCGA 696
DB 719 CCCCTACTGTCCCGTGTTCGCAATGGGACCTCGTGCCCAAGCTGGAGGGACCTTCGA 778
QY 697 GGACCTGCGTGTGCTGGGTGCTCTGTAGGCATCAGAGTTCACCTGGGATTTGTGACCTGGA 756
DB 779 GGACCTGCGTGTGCTGGGTGCTCTGTAGGCATCAGAGTTCACCTGGGATTTGTGACCTGGA 838
QY 757 CACCGGGACTGTGCTGCTGCTGCTACTACTCTTCAGCTGAGGAGAGAGCTACAA 816
DB 839 CACCGGGACTGTGCTGCTGCTGCTACTACTCTTCAGCTGAGGAGAGAGCTACAA 898
QY 817 CTTAGGACAGCACTCACTGCTGGGAGCAACCGGCTGTGGAGCCCGCACTTGTCTCA 876
DB 899 CTTAGGACAGCACTCACTGCTGGGAGCAACCGGCTGTGGAGCCCGCACTTGTCTCA 958
QY 877 GCTATATGAATTCGCTTCGACATCTCTGTCACCGGAGAGAGAGTTCGGGCTCAT 936
DB 959 GCTATATGAATTCGCTTCGACATCTCTGTCACCGGAGAGAGTTCGGGCTCAT 1018
QY 937 CCCACGCGCTGACACCTGGGACCGGGGAGCTTGGCTGGGCTGTGACCTTTTCTG 996
DB 1019 CCCACGCGCTGACACCTGGGACCGGGGAGCTTGGCTGGGCTGTGACCTTTTCTG 1078
QY 997 TGACCTGCTACTGTGTATGTGATAGAGAGCCCACTTCTACTGGAGGACAAAGTATGA 1056
DB 1079 TGACCTGCTACTGTGTATGTGATAGAGAGCCCACTTCTACTGGAGGACAAAGTATGA 1138
QY 1057 GGAGGCCAAGCCCGGAGAGCAACCGGCACTCTGTGTGGAGGAGCTGGCCCTTGCAATC 1116
DB 1139 GGAGGCCAAGCCCGGAGAGCAACCGGCACTCTGTGTGGAGGAGCTGGCCCTTGCAATC 1198
QY 1117 CCAAGCCGAGCTGGCCGAGTGCCTCAGACGGAGCTCAGCACTGCACCCCAAGCCCACTGC 1176
DB 1199 CCAAGCCGAGCTGGCCGAGTGCCTCAGACGGAGCTCAGCACTGCACCCCAAGCCCACTGC 1258
QY 1177 TGCTGGGAGTGCAGACACAGAGATGGCCCTGTCCAGTTCCTGACACCCCACTGGCC 1236
DB 1259 TGCTGGGAGTGCAGACACAGAGATGGCCCTGTCCAGTTCCTGACACCCCACTGGCC 1318
QY 1237 AACCCATTCCGGGAGCCCTGAGCCG-TTCCTGCTGTGTTGAGA-----GTTGGGGG 1286
DB 1319 AACCCATTCCGGGAGCCCTGAGCCGTTCCCTGCTGTGTTGAGAGAGAGGGGCTGGG 1378
QY 1287 CTGGGAAGGGGGGGCCCTGCTGGGATCTCAAGGATGAGGCCCAAGCATGGA 1340
DB 1379 AAGGAAGGACCCCTGCCCTGCCGAGCAAGCAAGGATGAGGCAACAGCAATGA 1432

RESULT 6

ADP49182

ID ADP49182 standard; DNA; 1452 BP.

XX AC

XX ADP49182;

XX XX

DT 26-AUG-2004 (first entry)

XX XX

DE Human P2X6 purinergic receptor DNA sequence for odour modulation.
XX
KW ds; gene; odour sensitivity; P2X purinergic receptor;
KW P2Y purinergic receptor; signal transduction pathway;
XX olfactory signalling; micro-array.
OS Homo sapiens.
PN WO2004047749-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037389.
XX
PR 21-NOV-2002; 2002US-0428140P.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Lucero M, Hegg C;
XX
XX WPI; 2004-460542/43.
XX
XX Modulating odor sensitivity in a subject, comprises administering a
PT composition comprising an agonist or antagonist of P2X or P2Y purinergic
PT receptor to the subject.
XX
XX Disclosure; SEQ ID NO 11; 108pp; English.
XX
XX The invention relates to a method of modulating (M1) odour sensitivity in
CC a subject, by administering a composition which is an agonist or
CC antagonist of a P2X or P2Y purinergic receptor. (M1) is useful for
CC modulating odour sensitivity in a subject (claimed). The compositions
CC used for modulating odour sensitivity in a subject are useful for
CC studying the signal transduction pathways related to olfactory signaling.
CC The compositions are also useful as reagents in micro-arrays or as
CC reagents to probe or analyze existing micro-arrays. This sequence
CC corresponds to the human P2X6 DNA sequence.
XX
XX Sequence 1452 BP; 316 A; 415 C; 442 G; 279 T; 0 U; 0 Other;

Query Match 43.6%; Score 1174; DB 12; Length 1452;
Best Local Similarity 97.2%; Pred. No. 3.2e-267;
Matches 1219; Conservative 0; Mismatches 25; Indels 10; Gaps 2;
QY 97 GTGGGCTCTCTCGCCAAAAGAGGCTACAGAGCGGACCTGGAAACCCAGTTTCCAT 156
DB 179 GTGGGCTCTCTCGCCAAAAGAGGCTACAGAGCGGACCTGGAAACCCAGTTTCCAT 238
QY 157 CATCACCAAACTCAAAGGGGTTTCGTCACATCAGATCAAGGAGCTTGAAACCGGCTGTG 216
DB 239 CATCACCAAACTCAAAGGGGTTTCGTCACATCAGATCAAGGAGCTTGAAACCGGCTGTG 298
QY 217 GATGTGGCCGACTTCGTGAAGCCACCTCAGGAGAGAGCGTTCCTCTTGGTGACAA 276
DB 299 GATGTGGCCGACTTCGTGAAGCCACCTCAGGAGAGAGCGTTCCTCTTGGTGACAA 358
QY 277 CTTCTCTGTGAGCCAGCCCAAGTTTCAGGGCAGATGCCAGAGCACCCGTCCTGCCACT 336
DB 359 CTTCTCTGTGAGCCAGCCCAAGTTTCAGGGCAGATGCCAGAGCACCCGTCCTGCCACT 418
QY 337 GGTCTAATCTGTGGTGTGACGAGGACTGCCCGAAGGGAGGAGGACACACAGCCACGG 396
DB 419 GGTCTAATCTGTGGTGTGACGAGGACTGCCCGAAGGGAGGAGGACACACAGCCACGG 478
QY 397 TGTAAAAACAGCCAGTGTGTGGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGGAG 456
DB 479 TGTAAAAACAGCCAGTGTGTGGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGGAG 538
QY 457 TTGGTGCCCAAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGCGCCAGGCGCCAGAA 516
DB 539 TTGGTGCCCAAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGCGCCAGGCGCCAGAA 598
QY 517 CTTACACATGTTCATCAAAAAACAGATCACCTTCCAGCAAGTTCACATCTCTTAAGTCCAA 576

Db 599 CTTTCACACTGTTTCATCAAAAACACAGTCACCTTCAGCAAGTTCAACTTCTCTAAGTCCAA 658
 Qy 577 TGCCTTGGAGACTGGGACCCACCTATTATTAAGCACTGCCGCTATGAACACCAATTGAG 636
 Db 659 TGCCTTGGAGACTGGGACCCACCTATTATTAAGCACTGCCGCTATGAACACCAATTGAG 718
 Qy 637 CCCTACTCTCCGCTGTTCCGATTTGGGACCTCTGTCGCAAGGCTGGAGGACCTTGA 696
 Db 719 CCCTACTCTCCGCTGTTCCGATTTGGGACCTCTGTCGCAAGGCTGGAGGACCTTGA 778
 Qy 697 GGACCTGGCGTTCCTGGCTGGCTCTGTAGGCATCAGAGTTCACTGGGATTTGACCTGGA 756
 Db 779 GGACCTGGCGTTCCTGGCTGGCTCTGTAGGCATCAGAGTTCACTGGGATTTGACCTGGA 838
 Qy 757 CACCGGGGACTCTGGCTGTGGCTCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACAA 816
 Db 839 CACCGGGGACTCTGGCTGTGGCTCTCACTACTCTTCCAGCTGCAGGAGAGAGCTACAA 898
 Qy 817 CTTTCAGGACGACCTCACTGTGGGACCAACCGGTGTGGAGGCCCGCACCTCTCTCAA 876
 Db 899 CTTTCAGGACGACCTCACTGTGGGACCAACCGGTGTGGAGGCCCGCACCTCTCTCAA 958
 Qy 877 GCTCTATGAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGAAAGTTGCGGCTCAT 936
 Db 959 GCTCTATGAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGAAAGTTGCGGCTCAT 1018
 Qy 937 CCCCAGCGCGTCACACTGGGACCGGGCAGCTTGGCTGGGCGTGTCACTTTTCTG 996
 Db 1019 CCCCAGCGCGTCACACTGGGACCGGGCAGCTTGGCTGGGCGTGTCACTTTTCTG 1078
 Qy 997 TGACCTGCTACTGCTGTATGTGATAGAGAGCCCATTTCTACTGGAGGACAAAGTATGA 1056
 Db 1079 TGACCTGCTACTGCTGTATGTGATAGAGAGCCCATTTCTACTGGAGGACAAAGTATGA 1138
 Qy 1057 GGAGGCGAGGCGCCGAAGACACCGCCAACTCTGTGTGGAGGAGCTGGCCCTTGCATC 1116
 Db 1139 GGAGGCGAGGCGCCGAAGACACCGCCAACTCTGTGTGGAGGAGCTGGCCCTTGCATC 1198
 Qy 1117 CCAAGCCCACTGGCGAGTGCTCAGACGAGCTCAGACCTGACACCCACGCGCACTGC 1176
 Db 1199 CCAAGCCCACTGGCGAGTGCTCAGACGAGCTCAGACCTGACACCCACGCGCACTGC 1258
 Qy 1177 TGTGGGAGTCAAGACACAGACACCAAGGATGGCCCTGTCCAAATTTGACACCCACTTGC 1236
 Db 1259 TGTGGGAGTCAAGACACAGACACCAAGGATGGCCCTGTCCAAATTTGACACCCACTTGC 1318
 Qy 1237 AACCCATTCCGGAGCTGTAGCCG-TTCCCTGCTGTTGAGA-----GTTGGGGG 1286
 Db 1319 AACCCATTCCGGAGCTGTAGCCGTTTCCCTGCTGTTGAGAAGGAGAGAGGGGCTGGGC 1378
 Qy 1287 CTGGGAAGGGCGGGGCCCTGCTGGGATCTCAAGGATGAGGCCCCAGCATGGA 1340
 Db 1379 AAGGAAGGACCCCTGCTGCCCTGCGAGCGAAGCAAGGATGAGGCAACAGCAATGA 1432

RESULT 7

ADP49174

ID ADP49174 standard; DNA; 1452 BP.

XX AC

XX ADP49174;

XX XX

DT 26-AUG-2004 (first entry)

XX XX

DE Rat P2X2 purinergic receptor DNA sequence for odour modulation.

XX XX

KW ds; gene; odour sensitivity; P2X purinergic receptor;

XX KW

KW P2Y purinergic receptor; signal transduction pathway;

XX KW

XX Olfactory signalling; micro-array.

OS Rattus sp.

XX XX

PN W02004047749-A2.

XX

PD 10-JUN-2004.

XX

PF 21-NOV-2003; 2003WO-US037389.

XX

PR 21-NOV-2002; 2002US-0428140P.

XX

PA (UTAH) UNIV UTAH RES FOUND.

XX

PI Lucero M, Hegg C;

XX

XX WPI; 2004-460642/43.

DR

Modulating odor sensitivity in a subject, comprises administering a composition comprising an agonist or antagonist of P2X or P2Y purinergic receptor to the subject.

PT

Disclosure; SEQ ID NO 3; 108pp; English.

PS

The invention relates to a method of modulating (M1) odour sensitivity in a subject, by administering a composition which is an agonist or antagonist of a P2X or P2Y purinergic receptor. (M1) is useful for modulating odour sensitivity in a subject (claimed). The compositions used for modulating odour sensitivity in a subject are useful for studying the signal transduction pathways related to olfactory signaling. The compositions are also useful as reagents in micro-arrays or as reagents to probe or analyze existing micro-arrays. This sequence corresponds to the rat P2X2 DNA sequence.

XX

Sequence 1452 BP; 316 A; 415 C; 442 G; 279 T; 0 U; 0 Other;

SQ

Query Match 43.6%; Score 1174; DB 12; Length 1452;

Best Local Similarity 97.2%; Pred. No. 3.2e-267;

Matches 1219; Conservative 0; Mismatches 25; Indels 10; Gaps 2;

Qy 97 GTGGGCTCTCTCGCCAAAAGGCTACCAAGGCGGAGCTGGAACCCAGTTTCCAT 156

Db 179 GTGGGCTCTCTCGCCAAAAGGCTACCAAGGCGGAGCTGGAACCCAGTTTCCAT 238

Qy 157 CATCAACAACTCAAGGGGTTTCCGTCACATCAAGAGCTTGGAAACCGGTGTG 216

Db 239 CATCAACAACTCAAGGGGTTTCCGTCACATCAAGAGCTTGGAAACCGGTGTG 298

Qy 217 GGATGTGGCGACTTCGTGAAGCCACTCAGGAGAGAACGTGTTCTTGTGTGACAA 276

Db 299 GGATGTGGCGACTTCGTGAAGCCACTCAGGAGAGAACGTGTTCTTGTGTGACAA 358

Qy 277 CTTCTTGTGACGCCACCCCAAGTTCAAGGACATGCCAGAGACCCGTCCTCCCACT 336

Db 359 CTTCTTGTGACGCCACCCCAAGTTCAAGGACATGCCAGAGACCCGTCCTCCCACT 418

Qy 337 GGCTAACTGCTGGGTGACAGGAGACTGCCCCGAAGGGAGGAGGCACACAGCCACGG 396

Db 419 GGCTAACTGCTGGGTGACAGGAGACTGCCCCGAAGGGAGGAGGCACACAGCCACGG 478

Qy 397 TGTAAAACAGGCCAGTGTGTGTTCAATGGGACCCACAGGACCTGTGAGTCTGGAG 456

Db 479 TGTAAAACAGGCCAGTGTGTGTTCAATGGGACCCACAGGACCTGTGAGTCTGGAG 538

Qy 457 TTGCTGCCCAAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGTCGCCCCAGAA 516

Db 539 TTGCTGCCCAAGTGGAGAGTGGCGTTGTGCCCTCGAGGCCCTGTGTCGCCCCAGAA 598

Qy 517 CTTCACTGTTTCATCAAAAACACAGTCACCTTCAGCAAGTTCACTTCTAAGTCAA 576

Db 599 CTTCACTGTTTCATCAAAAACACAGTCACCTTCAGCAAGTTCACTTCTAAGTCAA 658

Qy 577 TGCCTTGGAGACCTGGGACCCCACTATTTTAAGCACTGCGGCTATGAACACCAATTGAG 636

Db 659 TGCCTTGGAGACCTGGGACCCCACTATTTTAAGCACTGCGGCTATGAACACCAATTGAG 718

Qy 637 CCCCTACTGTCCCGTGTTCGCAATTTGGGACCTGCTGGCCAAAGGCTGGAGGACCTTGA 696

Db 719 CCCCTACTGTCCTGCTGTTCCGCAATTTGGGACCTCTGTCGCCAAGCTGGAGGACCTTCGA 778
QY 697 GCACCTGGGTTGCTGGGTGGCTCTGTAGGATCAGAGTTTCACTGGGATTTGACCTGGA 756
Db 779 GGACCTGGGTTGCTGGGTGGCTCTGTAGGATCAGAGTTTCACTGGGATTTGACCTGGA 838
QY 757 CACCGGGGACTCTGGCTGCTGGCTCTCACTACTCTCTCCAGCTGCAGGAGAGAGCTCAA 816
Db 839 CACCGGGGACTCTGGCTGCTGGCTCTCACTACTCTCTCCAGCTGCAGGAGAGAGCTCAA 898
QY 817 CTTTACGACAGCACTCACTGTGGGACCAACCGGCTGTGGAGCCCGACCTGCTCAA 876
Db 899 CTTTACGACAGCACTCACTGTGGGACCAACCGGCTGTGGAGCCCGACCTGCTCAA 958
QY 877 GCTCTATGGAATCCGCTTCGACATCCTCTGTACCGGGCAGGAGGAGTTTCGGGCTCAT 936
Db 959 GCTCTATGGAATCCGCTTCGACATCCTCTGTACCGGGCAGGAGGAGTTTCGGGCTCAT 1018
QY 937 CCCACGGCCGTCACACTGGGACCCGGGGAGCTTGGCTGGGGGTGTGTCACCTTTTCTG 996
Db 1019 CCCACGGCCGTCACACTGGGACCCGGGGAGCTTGGCTGGGGGTGTGTCACCTTTTCTG 1078
QY 997 TGACCTGCTACTGCTGTATGTGGATAGAGAGCCCATTTCTACTGGAGGACAAAGTATGA 1056
Db 1079 TGACCTGCTACTGCTGTATGTGGATAGAGAGCCCATTTCTACTGGAGGACAAAGTATGA 1138
QY 1057 GGAGGCCAAGGCCCGAAGCAACCGCAACTCTGTGTGGAGGAGCTGGCCCTTTCGATC 1116
Db 1139 GGAGGCCAAGGCCCGAAGCAACCGCAACTCTGTGTGGAGGAGCTGGCCCTTTCGATC 1198
QY 1117 CCACGCCGACTGGCCGAGTGCCTCAGACGAGCTCAGCCTGCACCCAGGCACTGC 1176
Db 1199 CCACGCCGACTGGCCGAGTGCCTCAGACGAGCTCAGCCTGCACCCAGGCACTGC 1258
QY 1177 TGCTGGGAGTCAGACACAGACACAGGATGGCCCTGTCCAGTTCCTGACACCCACTTGCC 1236
Db 1259 TGCTGGGAGTCAGACACAGACACAGGATGGCCCTGTCCAGTTCCTGACACCCACTTGCC 1318
QY 1237 AACCCATTCGGGAGCTGTAGCG- TTCCCTGCTGGTTGAGA-----GTTGGGG 1286
Db 1319 AACCCATTCGGGAGCTGTAGCGTTTCCCTGCTGGTTGAGAAGAGAGGAGGCGCTGGC 1378
QY 1287 CTGGGAAGGGGGGCCCTGCTGGGATCTCAAGGATGAGGCCCCAGCATGA 1340
Db 1379 AAGGAGGACCCCTGCCCTGCGAGCGAAGCAGGATGAGGCAACAGCATGA 1432

RESULT 8

ADP49176

ID ADP49176 standard; DNA; 1452 Bp.

XX AC ADP49176;

XX AC ADP49176;

DT 26-AUG-2004 (first entry)

DE Human P2X3 purinergic receptor DNA sequence for odour modulation.

XX ds; gene; odour sensitivity; P2X purinergic receptor;

XX P2Y purinergic receptor; signal transduction pathway;

XX olfactory signalling; micro-array.

XX OS Homo sapiens.

XX XX

FN WO2004047749-A2.

PD 10-JUN-2004.

XX XX

PF 21-NOV-2003; 2003WO-US037389.

XX XX

PR 21-NOV-2002; 2002US-0428140P.

XX XX

PA (UTAH) UNIV UTAH RES FOUND.

XX XX

PI Lucero M, Hegg C;
XX WPI; 2004-460642/43.
XX Modulating odor sensitivity in a subject, comprises administering a
PT composition comprising an agonist or antagonist of P2X or P2Y purinergic
PT receptor to the subject.
XX Disclosure; SEQ ID NO 5; 108pp; English.
XX
CC The invention relates to a method of modulating (M1) odour sensitivity in
CC a subject, by administering a composition which is an agonist or
CC antagonist of a P2X or P2Y purinergic receptor. (M1) is useful for
CC modulating odour sensitivity in a subject (claimed). The compositions
CC used for modulating odour sensitivity in a subject are useful for
CC studying the signal transduction pathways related to olfactory signaling.
CC The compositions are also useful as reagents in micro-arrays or as
CC reagents to probe or analyze existing micro-arrays. This sequence
CC corresponds to the human P2X3 DNA sequence.
XX
SQ Sequence 1452 Bp; 316 A; 415 C; 442 G; 279 T; 0 U; 0 Other;

Query Match 43.6%; Score 1174; DB 12; Length 1452;
Best Local Similarity 97.2%; Pred. No. 3.2e-267;
Matches 1219; Conservative 0; Mismatches 25; Indels 10; Gaps 2;

QY 97 GTGGGCTCTCTCGCCAAAAGGCTACAGGAGCGGACCTGGAAACCCAGTTTCCAT 156
Db 179 GTGGGCTCTCTCGCCAAAAGGCTACAGGAGCGGACCTGGAAACCCAGTTTCCAT 238
QY 157 CATCACCAAACTCAAGGGGTTTCGTCACATCAGATCAAGGAGCTTGAACCGGCTGTG 216
Db 239 CATCACCAAACTCAAGGGGTTTCGTCACATCAGATCAAGGAGCTTGAACCGGCTGTG 298
QY 217 GGATGTGGCGGACTCTCGTGAAGCCACCTCAGGAGAGAACCTGTTCCTTCTTGGTGACCAA 276
Db 299 GGATGTGGCGGACTCTCGTGAAGCCACCTCAGGAGAGAACCTGTTCCTTCTTGGTGACCAA 358
QY 277 CTTCTCTGTGACCCAGCCAGCCAAAGTTTCAGGCGAGATGCCAGAGACCCGTCGTCCTCACT 336
Db 359 CTTCTCTGTGACCCAGCCAGCCAAAGTTTCAGGCGAGATGCCAGAGACCCGTCGTCCTCACT 418
QY 337 GCCTAACTCTCGGCTCGACGAGGACTGCCCCGAGGAGGAGGACACACAGCCACGG 396
Db 419 GGCTAACTCTCGGCTCGACGAGACTGCCCCGAGGAGGAGGAGGACACACAGCCACGG 478
QY 397 TGTAAAAACAGCCAGCTGTGGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGGAG 456
Db 479 TGTAAAAACAGCCAGCTGTGGTGTTCATATGGGACCCACAGGACCTGTGAGATCTGGAG 538
QY 457 TTGGTGGCCAGTGGAGAGTGGCGTTGTCCTTCAGAGCCCTGCTGGCCCGCCAGCCAGAA 516
Db 539 TTGGTGGCCAGTGGAGAGTGGCGTTGTCCTTCAGAGCCCTGCTGGCCCGCCAGCCAGAA 598
QY 517 CTTCACTCTGTTCATCAAAAACACAGTCACTTCAGCAAGTTCAACTTCTCTAAGTCCAA 576
Db 599 CTTCACTCTGTTCATCAAAAACACAGTCACTTCAGCAAGTTCAACTTCTCTAAGTCCAA 658
QY 577 TGGCTTGGAGACCTGGGACCCACCTATTTAAGCACTGCGGCTATGACCAATTCAG 636
Db 659 TGGCTTGGAGACCTGGGACCCACCTATTTAAGCACTGCGGCTATGACCAATTCAG 718
QY 637 CCCCTACTGTCCCGTGTTCGCAATTTGGGACCTCGTGGCCCAAGGCTGGAGGACCTTCGA 696
Db 719 CCCCTACTGTCCCGTGTTCGCAATTTGGGACCTCGTGGCCCAAGGCTGGAGGACCTTCGA 778
QY 697 GGACCTGGGTTGCTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGGA 756
Db 779 GGACCTGGGTTGCTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGGA 838
QY 757 CACCGGGGACTCTGGCTGCTGCTCACTACTCTCTTCCAGCTGCAGGAGAGAGCTACAA 816
Db 839 CACCGGGGACTCTGGCTGCTGCTCACTACTCTCTTCCAGCTGCAGGAGAGAGCTACAA 898

QY 817 CTTTCAGGACAGCACTCACTGGTGGAGCAACCGGGTGGAGGCCCGCACCTCTCAA 876
 DB 899 CTTTCAGGACAGCACTCACTGGTGGAGCAACCGGGTGGAGGCCCGCACCTCTCAA 958
 QY 877 GCTCTATGAATCCGCTTCGACATCTCTGTCACCCGGGAGGAGGAGGAGTTCGGGCTCAT 936
 DB 959 GCTCTATGAATCCGCTTCGACATCTCTGTCACCCGGGAGGAGGAGGAGTTCGGGCTCAT 1018
 QY 937 CCCACGGCGGTACACTGGGACCCCGGGCAGCTTGGCTGGGGGTGGTCACTTTTCTG 996
 DB 1019 CCCACGGCGGTACACTGGGACCCCGGGCAGCTTGGCTGGGGGTGGTCACTTTTCTG 1078
 QY 997 TGACCTGCTACTCTGTATGTGATAGAGAGCCCAATTTCTACTGGAGGACAAAGTATGA 1056
 DB 1079 TGACCTGCTACTCTGTATGTGATAGAGAGCCCAATTTCTACTGGAGGACAAAGTATGA 1138
 QY 1057 GGAGGCGAAGGCCCCGAAAGCAACCGCCAACTCTGTGTGGAGGAGCTGGCCCTTGCATC 1116
 DB 1139 GGAGGCGAAGGCCCCGAAAGCAACCGCCAACTCTGTGTGGAGGAGCTGGCCCTTGCATC 1198
 QY 1117 CCAAGCCGACTGGCGAGTGCTCAGACGGAGCTCAGACCTGCACCCACGCGCACTGC 1176
 DB 1199 CCAAGCCGACTGGCGAGTGCTCAGACGGAGCTCAGACCTGCACCCACGCGCACTGC 1258
 QY 1177 TGTGGAGTACAGACAGACAGGATGGCCCTGTCCAAGTCTGACACCCACTTGC 1236
 DB 1259 TGTGGAGTACAGACAGACAGGATGGCCCTGTCCAAGTCTGACACCCACTTGC 1318
 QY 1237 AACCCATTCGGGAGCTGTAGCGG-TTCCCTGCTGTTGAGA-----GTTGGGG 1286
 DB 1319 AACCCATTCGGGAGCTGTAGCGGTTCCCTGCTGTTGAGAAGAGAGGCGGTGGGC 1378
 QY 1287 CTGGGAAGCGGGGGCCCTGCTGGGATCTCAAGGATGAGGCCCGCCAGCATGA 1340
 DB 1379 AAGGAAGGCCCTGCTGCCCTGCCGAGCAAGCAAGATGAGGCAACAGCAATGA 1432
 RESULT 9
 AAD04978
 ID AAD04978 standard; cDNA; 1360 BP.
 AC AAD04978;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE Human purinergic receptor P2X6 cDNA.
 XX
 KW Human; purinergic receptor; P2X6; antidepressant; vulnerability; hypotensive;
 KW anticonvulsant; antiinflammatory; therapy; nervous system disorder;
 KW epilepsy; pain; depression; neurodegenerative disorder; cystic fibrosis;
 KW neuromuscular disease; reproductive system disorder; hypertension;
 KW peripheral vascular disease; immune system disorder; chronic bronchitis;
 KW irritable bowel disorder; premature ejaculation; asthma; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..14
 FT /tag= a
 FT /note= "5' flanking sequence including BamHI restriction
 FT site"
 FT CDS 16..1341
 FT /tag= b
 FT /product= "Human P2X6 receptor protein"
 FT 1344..1360
 FT misc_feature
 FT /tag= c
 FT /note= "3' flanking sequence containing Not I restriction
 FT site"
 XX
 PN US6214581-B1.
 XX
 PD 10-APR-2001.

XX 13-NOV-1998; 98US-001911136.
 XX
 XX 16-JAN-1998; 98US-00008185.
 PR 16-JAN-1998; 98US-00008526.
 PR 16-JAN-1998; 98US-0071298P.
 PR 16-JAN-1998; 98US-0071669P.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 XX Lynch KJ, Burgard EC, Van Biesen T;
 PI WPI; 2001-315459/33.
 DR P-PSDB; AAE01141.
 XX
 PT Novel isolated polynucleotide encoding human purinergic P2X3 receptor
 PT polypeptide useful for identifying potentially therapeutic compounds that
 PT modulate or otherwise interact with P2X containing receptors.
 XX
 XX Example 9; Fig 8; 53pp; English.
 XX
 CC The present sequence is a cDNA encoding human P2X6 purinergic receptor
 CC protein. P2X receptors are ligand-gated ion channels while P2Y receptors
 CC operate generally through a G-protein coupled system. P2X purinoreceptor
 CC drugs are potential therapeutic agents in several disorders including
 CC central nervous system or peripheral nervous system conditions, e.g.;
 CC epilepsy, pain, depression, neurodegenerative disorders, disorders of the
 CC skeletal muscle such as neuromuscular diseases, disorders of the
 CC reproductive system, asthma, peripheral vascular disease, hypertension,
 CC immune system disorders, irritable bowel disorder, premature ejaculation,
 CC cystic fibrosis and chronic bronchitis. P2Y purinoreceptors mediate the
 CC activity of extracellular nucleotide triphosphates to regulate chloride
 CC secretion in human airway epithelia
 XX
 SQ Sequence 1360 BP; 284 A; 403 C; 412 G; 261 T; 0 U; 0 Other;
 Query Match 43.2%; Score 1162.4; DB 4; Length 1360;
 Best Local Similarity 99.9%; Pred. No. 1.7e-264;
 Matches 1163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 97 GTGGGCTCTCTCCCAAAAAGGCTACAGGAGCGGAGCTCGAAACCCAGTTTCCAT 156
 DB 180 GTGGGCGCTCTCCCAAAAAGGCTACAGGAGCGGAGCTCGAAACCCAGTTTCCAT 239
 QY 157 CATCACCAACTCAAGGGGTTTCCGTCACATCAGATCAAGGAGCTTGGAAACCGGCTGTG 216
 DB 240 CATCACCAACTCAAGGGGTTTCCGTCACATCAGATCAAGGAGCTTGGAAACCGGCTGTG 299
 QY 217 GGATGTGGCCGACTTGTGAAGCCACTCAGGAGAGAGCACTGTCTTCTTGTGACCAA 276
 DB 300 GGATGTGGCCGACTTGTGAAGCCACTCAGGAGAGAGAGCACTGTCTTCTTGTGACCAA 359
 QY 277 CTTCTTGTGTAGCCGAGCCCAAGTTCAGGGCAGATGCCAGAGCACCCGTCCTCCCACT 336
 DB 360 CTTCTTGTGTAGCCGAGCCCAAGTTCAGGGCAGATGCCAGAGCACCCGTCCTCCCACT 419
 QY 337 GGCTAACTGTGGTTCGACGAGGAGTGCCTCCGAGGGAGGAGGAGGCACACAGCCAGCG 396
 DB 420 GGCTAACTGTGGTTCGACGAGGAGTGCCTCCGAGGGAGGAGGAGGCACACAGCCAGCG 479
 QY 337 TGTAAAAACAGCCAGTGTGTGGTTCATATGGAGCCACAGGACCTGTGTAGATCTGGAG 456
 DB 480 TGTAAAAACAGCCAGTGTGTGGTTCATATGGAGCCACAGGACCTGTGTAGATCTGGAG 539
 QY 457 TTGGTGGCCAGTGGAGTGGCGTTGTGCCCTCCAGGCCCTGTGGCCAGGCCAGAA 516
 DB 540 TTGGTGGCCAGTGGAGTGGCGTTGTGCCCTCCAGGCCCTGTGGCCAGGCCAGAA 599
 QY 517 CTTTCACTGTTCATCAAAAAACAGATCACCTTCAGCAAGTTCACCTTCTTAAGTCCAA 576
 DB 600 CTTTCACTGTTCATCAAAAAACAGATCACCTTCAGCAAGTTCACCTTCTTAAGTCCAA 659
 QY 577 TGCCTTGGAGACCTGGGACCCCACTATTTTAAGCACTGCCGCTATGNACCACATTCAG 636

Db 660 TGCCCTGGAGACCTGGAGACCCACCTATTTTAAGCACTCCCGCTATGAACCAATTCAG 719
 QY 637 CCCTACTGTCCCGTGTTCGGCATTTGGGACCTCTGTGGCAAGGCTGGAGGACCTTGA 696
 Db 720 CCCTACTGTCCCGTGTTCGGCATTTGGGACCTCTGTGGCAAGGCTGGAGGACCTTGA 779
 QY 697 GACCTGGCGTGTCTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGA 756
 Db 780 GGACCTGGCGTGTCTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGA 839
 QY 757 CACCGGGGACTCTGGTGTGGCTCCTCACTCTCTCACTCTCACTCTCACTCTCACTCTCA 816
 Db 840 CACCGGGGACTCTGGTGTGGCTCCTCACTCTCTCACTCTCTCACTCTCTCACTCTCA 899
 QY 817 CTTTACGACAGCACTCACTGTGGAGCAACCGGCTGTGGAGCCCGACCTCTCA 876
 Db 900 CTTTACGACAGCACTCACTGTGGAGCAACCGGCTGTGGAGCCCGACCTCTCA 959
 QY 877 GTCTATGAATCCGCTTCGACATCTCTGTCACTCTCTCACTCTCTCACTCTCTCA 936
 Db 960 GTCTATGAATCCGCTTCGACATCTCTGTCACTCTCTCACTCTCTCACTCTCTCA 1019
 QY 937 CCCCAGCGCGTCACTCTGGGACCCGGGACCTTGGCTGGCGTGGTCACTTTTCTG 996
 Db 1020 CCCCAGCGCGTCACTCTGGGACCCGGGACCTTGGCTGGCGTGGTCACTTTTCTG 1079
 QY 997 TGACCTGTCTCTGT 1056
 Db 1080 TGACCTGTCTCTGT 1139
 QY 1057 GGAGGCCAAGGCCCGAAGCAACCGCACTCTGTGTGGAGGAGCTGGCCCTTGCATC 1116
 Db 1140 GGAGGCCAAGGCCCGAAGCAACCGCACTCTGTGTGGAGGAGCTGGCCCTTGCATC 1199
 QY 1117 CCAAGCCGACTGGCGGAGTGTCTCAGAGGAGTCTAGCACTTGCACCCAGCGGCTGTC 1176
 Db 1200 CCAAGCCGACTGGCGGAGTGTCTCAGAGGAGTCTAGCACTTGCACCCAGCGGCTGTC 1259
 QY 1177 TGCTGGAGTCTAGAC 1236
 Db 1260 TGCTGGAGTCTAGAC 1319
 QY 1237 AACCATTCGGGAGCTGTAGCC 1260
 Db 1320 AACCATTCGGGAGCTGTAGCC 1343

RESULT 10

AAV61832
 ID AAV61832 standard; cDNA; 1293 BP.

AC AAV61832;

DT 28-APR-1999 (first entry)

XX Coding sequence for human p53 regulated protein, P2XM.

KW Human; p53 regulated protein; P2XM; ATP receptor; RP-2 protein;
 KW thymocyte; apoptosis; tumour-suppressor gene; rhabdoid sarcoma;
 KW anticancer drug; ss.

OS Homo sapiens.

PN WO9842835-A1.

PD 01-OCT-1998.

PF 18-MAR-1998; 98WO-JP001146.

PR 26-MAR-1997; 97JP-00093044.

PA (SAKA) OTSUKA PHARM CO LTD.

XX Tokino T, Nakamura Y;
 XX WPI; 1998-532006/45.
 XX P-PSDB; AAW76434.
 PT Human gene P2XM whose transcription is induced by p53 - useful, e.g. for
 PT diagnostic purposes and in development of new anticancer drugs.
 XX Claim 2; Page 22-23; 43pp; Japanese.
 CC This sequence represents the coding sequence for the P2XM protein of the
 CC invention. The protein is significantly homologous to: (i) the P2X family
 CC of ATP receptors, and (ii) RP-2 protein which is expressed in thymocytes
 CC during apoptosis. Transcription of the genes is specifically regulated by
 CC the tumour-suppressor gene p53. The P2XM gene is specifically expressed
 CC in skeletal muscle and has been localised to chromosome 22q11, an area
 CC where mutation and sequence losses frequently occur in rhabdoid sarcomas.
 CC The genes may be used for diagnostic purposes (e.g. by detecting changes
 CC occurring in the gene in sarcomas), using probes and primers containing
 CC or derived from all or part of the genes. The genes may further be used
 CC in the development of new anticancer drugs

XX SQ Sequence 1293 BP; 271 A; 379 C; 389 G; 254 T; 0 U; 0 Other;

Query Match 42.9%; Score 1155.8; DB 2; Length 1293;

Best Local Similarity 99.8%; Pred. No. 6.1e-263;

Matches 1157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 97 GTGGGCTCTCTCCGCAAAAGGCTTACAGGAGCGGACCTGGAAACCCAGTTTCCAT 156
 Db 135 GTGGGCGCTCTCCGCAAAAGGCTTACAGGAGCGGACCTGGAAACCCAGTTTCCAT 194
 QY 157 CATCACCAACTCAAGGGGTTTCGTCACTCAGATCAAGGAGCTTGGAAACCGGTGTG 216
 Db 195 CATCACCAACTCAAGGGGTTTCGTCACTCAGATCAAGGAGCTTGGAAACCGGTGTG 254
 QY 217 GGATGTGGCGGATTCGTGAAGCCACCTCAGGAGAGAACGTGTCTTCTTGGTACCACAA 276
 Db 255 GGATGTGGCGGATTCGTGAAGCCACCTCAGGAGAGAACGTGTCTTCTTGGTACCACAA 314
 QY 277 CTTCTCTGTGACGCCAGCCAGTTTCAGGCGAGATGCCAGAGACCCGTCGTCCTCCAT 336
 Db 315 CTTCTCTGTGACGCCAGCCAGTTTCAGGCGAGATGCCAGAGACCCGTCGTCCTCCAT 374
 QY 337 GGCTAACTGTGGTCTGACGAGGACTGCCCCAAGGGAGGAGGCACACACAGCCACGG 396
 Db 375 GGCTAACTGTGGTCTGACGAGGACTGCCCCAAGGGAGGAGGCACACACAGCCACGG 434
 QY 397 TGTAATAACAGGCCAGT 456
 Db 435 TGTAATAACAGGCCAGT 494
 QY 457 TTGTGCCCCGCTGGAGTGGGT 516
 Db 495 TTGTGCCCCGCTGGAGTGGGT 554
 QY 517 CTTTACACTGTTTCATCAAAAACACAGTCACTTCAAGTTCAGCAAGTTCAACTTCTTAA 576
 Db 555 CTTTACACTGTTTCATCAAAAACACAGTCACTTCAAGTTCAGCAAGTTCAACTTCTTAA 614
 QY 577 TGCCTTGGAGACTGGGACCCCACTATTTTAAAGCACTGCCGCTATGAACCAATTCAG 636
 Db 615 TGCCTTGGAGACTGGGACCCCACTATTTTAAAGCACTGCCGCTATGAACCAATTCAG 674
 QY 637 CCCCCTACTGTCCCGTGTTCGCAATTTGGGACCTCTGTGGCCAAAGGCTGGAGGACCTTCCA 696
 Db 675 CCCCCTACTGTCCCGTGTTCGCAATTTGGGACCTCTGTGGCCAAAGGCTGGAGGACCTTCCA 734
 QY 697 GGACCTGGCGTGTCTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGGA 756
 Db 735 GGACCTGGCGTGTCTGGGTGGCTCTGTAGGATCAGAGTTCACTGGGATTTGACCTGGA 794

QY	757	CACGGGAGCTCTGGCTGCTGGCTCCTACTCTCTTCCAGCTGCAGGAGAGAGCTACAA	816
Db	795	CACGGGAGCTCTGGCTGCTGGCTCCTACTCTCTTCCAGCTGCAGGAGAGAGCTACAA	854
QY	817	CTTCAGGACAGCCACTCACTGGTGGAGCAACCGGGTGTGAGGCCCGCCACCTGCTCAA	876
Db	855	CTTCAGGACAGCCACTCACTGGTGGAGCAACCGGGTGTGAGGCCCGCCACCTGCTCAA	914
QY	877	GCTCTATGGAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGGAAGTTGCGGCTCAT	936
Db	915	GCTCTATGGAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGGAAGTTGCGGCTCAT	974
QY	937	CCCACGGCCGTCACTGGGACCGGGCAGCTTGGCTGGCGGTGTCACCTTTTCTG	996
Db	975	CCCACGGCCGTCACTGGGACCGGGCAGCTTGGCTGGCGGTGTCACCTTTTCTG	1034
QY	997	TGACCTGCTACTGCTGTATGTGGATAGAGAGCCCATTTCTACTGGAGGAGCTGGCCCTTGCA	1056
Db	1035	TGACCTGCTACTGCTGTATGTGGATAGAGAGCCCATTTCTACTGGAGGAGCTGGCCCTTGCA	1094
QY	1057	GGAGGCCAAGGCCCGCAAGCAACCGCCAACTCTGTGTGGAGGAGCTGGCCCTTGCA	1116
Db	1095	GGAGGCCAAGGCCCGCAAGCAACCGCCAACTCTGTGTGGAGGAGCTGGCCCTTGCA	1154
QY	1117	CCAAGCCGAGTGGCGGAGTGCTCAGACGGAGCTCAGCAGCTGACCCAGGCGCACTGC	1176
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XX			
DT	12-AUG-2004 (first entry)		
XX			
DE	Human secreted protein encoding sequence SEQ ID #206.		
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KW	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;		
KW	cancer; inflammatory; immune; ds; human secreted protein.		
OS	Homo sapiens.		
XX			
PN	WC004035732-A2.		
XX			
PD	29-APR-2004.		
XX			
PF	28-AUG-2003; 2003WO-US025780.		
XX			
PR	29-AUG-2002; 2002US-0406576P.		
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PR	08-AUG-2003; 2003US-0493573P.	
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XX	(FIVE)- FIVE PRIME THERAPEUTICS INC.	
PA	Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;	
XX	Halenbeck RF, Huang MM, Kothakota S, Linnemann T;	
PI	Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;	
XX	WPI; 2004-348438/32.	
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PT	New nucleic acid molecule for diagnosing, preventing or treating diseases	
PT	such as proliferative (e.g. cancer), inflammatory, immune, metabolic,	
PT	genetic, bacterial and viral diseases.	
PS	Claim 1; SEQ ID NO 206; 428pp; English.	
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CC	The present invention relates to an isolated nucleic acid molecule	
CC	encoding a polypeptide which is believed to be cytostatic,	
CC	antiinflammatory, immunosuppressive, antibacterial and virucidal. The	
CC	composition and methods are useful for diagnosing, preventing and	
CC	treating diseases such as proliferative (e.g. cancer), inflammatory,	

CC immune, metabolic, genetic, bacterial and viral diseases. The present
 CC sequence represents a human secreted protein encoding sequence. The
 CC present sequence is available on WIPWEB and is not in the specification.
 XX
 SQ Sequence 900 BP; 182 A; 251 C; 288 G; 179 T; 0 U; 0 Other;

Query Match 25.2%; Score 678.4; DB 12; Length 900;
 Best Local Similarity 89.4%; Pred. No. 4.1e-150;
 Matches 792; Conservative 0; Mismatches 1; Indels 93; Gaps 2;
 QY 97 GTGGGCTCTCTCCGCAAAAGGCTTACAGAGCGGACCTGGACCCACCTGTTTCCAT 156
 Db 108 GTGGGCTCTCTCCGCAAAAGGCTTACAGAGCGGACCTGGACCCACCTGTTTCCAT 167
 QY 157 CATCAACAACCTAAAGGGGTTTCGTCTACTCAGATCAAGAGCTTGGAAACCGGCTGTG 216
 Db 168 CATCAACAACCTAAAGGGGTTTCGTCTACTCAGATCAAGAGCTTGGAAACCGGCTGTG 227
 QY 217 GGATGGCGGACTTCGTGAAGCCCTCAGAGGAGACGTTCTTCTTGGTGACCA 276
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 Db 288 CTTCTTGTGACGCCCAAGTTCAGGGCAGATGCCAGAGCACCCGTCGTCCTCACT 347
 QY 337 GGCTAACTGCTGGTTCGACGAGACTGCCCGAAGGGAGGAGGACACACAGCCACGG 396
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 QY 397 TGTAAAAACAGCCGAGTGTGGTGTCAATGGGACCCACAGGACCTGTGAGATCTGGAG 456
 Db 408 TGTAAAAACAGCCGAGTGTGGTGTCAATGGGACCCACAGGACCTGTGAGATCTGGAG 467
 QY 457 TTGGTCCGAGTGAGAGTGCGTGTGTCCTTCGAGGCCCTGTGTCGCCAGGCCAGAA 516
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 Db 567 ----- 566
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 XX AA118520 standard; DNA; 569 BP.
 AC AA118520;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Probe #8453 for gene expression analysis in human cervical cell sample.
 CC Probe: human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer; ss.
 XX
 OS Homo sapiens.
 PN W0200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001W0-US000670.
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 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234887P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 FT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 XX Claim 25; SEQ ID NO 8453; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging of
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
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 SQ Sequence 569 BP; 131 A; 167 C; 167 G; 104 T; 0 U; 0 Other;
 Query Match 21.1%; Score 567.4; DB 4; Length 569;
 Best Local Similarity 99.8%; Pred. No. 6.2e-124;
 Matches 568; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1497 ACCTGTATTGAGGGCTCCGACTGCATGTGCAGGGGCTCCTGCTGGTCTGGGCTGGA 1556
 Db 569 ACCTGTATTGAGGGCTCCGACTGCATGTGCAGGGGCTCCTGCTGGTCTGGGCTGGA 510
 QY 1557 GGTCTCTCCAGTGTCTCTGCCAGTGTCTTAGCAGAGGTATGCTTACAGCTGTC 1616
 Db 509 GGTCTCTCCAGTGTCTCTGCCAGTGTCTTAGCAGAGGTATGCTTACAGCTGTC 450
 QY 1617 AGCAGACACCTCTGCTGCTGGTCTCTGCCAGTGTCTTAGCAGAGGTATGCTTACAGCTGTC 1676
 Db 449 AGCAGACACCTCTGCTGCTGGTCTCTGCCAGTGTCTTAGCAGAGGTATGCTTACAGCTGTC 390
 QY 1677 AGGTAGAGACCCACCTCTGCCAGTGTCTTAGCAGAGGTATGCTTACAGCTGTC 1736
 Db 389 AGGTAGAGACCCACCTCTGCCAGTGTCTTAGCAGAGGTATGCTTACAGCTGTC 330
 QY 1737 GCAGGGCAGAGAGGAGTATGGGGAGGGGATGTTTTCAGCTTCTCTGGTCTGTA 1796

Db 269 TGCCCCAGGAGAGTCCTAATCTAGGAATGGGTTGGAGTAGGAGATATATCCACCTCCCT 210
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QY 1977 GCAGGGCTAAGTTGGTGATCATTGGGTCTTCAGGACCTTCTATATCCCTCCGTAAAC 2036
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Job time : 1297.69 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 12:30:45 ; Search time 11523.5 Seconds
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Perfect score: 2693
Sequence: 1 ttgtgtactcatgtgccgcg.....aaaaaaaaaaaaaaaaaaaaa 2693

Scoring table: IDENTITY NUC
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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053459

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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13: gb.un.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2558.8	95.0	3554	CQ730055	CQ730055 Sequence
3	2517.2	93.5	3552	AB002058	AB002058 Homo sapi
4	2382.8	88.5	2578	BC064805	BC064805 Homo sapi
5	1592.6	59.1	147086	AC002472	AC002472 Homo sapi
6	1592.6	59.1	162470	AC007664	AC007664 Homo sapi
7	1552.6	57.7	28984	AB002059	AB002059 Homo sapi
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10	1336.8	49.6	1517	CR456535	CR456535 Homo sapi
11	1204.4	44.7	2034	BC063553	BC063553 Homo sapi
12	1174	43.6	1452	AF065385	AF065385 Homo sapi
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17	729.2	27.1	1458	RNP2X6	RNP2X6 R.norvegicu
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C 21	567.4	21.1	569	6	CQ177794	Sequence
C 22	567.4	21.1	569	6	CQ225557	Sequence
C 23	567.4	21.1	569	6	CQ263572	Sequence
C 24	567.4	21.1	569	6	CQ300643	Sequence
C 25	567.4	21.1	569	6	CQ337952	Sequence
C 26	449.6	16.7	175167	2	AC116044	Papio ham
C 27	377	14.0	577	6	CQ073194	Sequence
C 28	377	14.0	577	6	CQ104037	Sequence
C 29	377	14.0	577	6	CQ142803	Sequence
C 30	377	14.0	577	6	CQ178299	Sequence
C 31	377	14.0	577	6	CQ226029	Sequence
C 32	377	14.0	577	6	CQ264110	Sequence
C 33	377	14.0	577	6	CQ301199	Sequence
C 34	377	14.0	577	6	CQ338447	Sequence
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C 36	296.2	11.0	2436	10	RNRNAP2X5	X92069 R.norvegicu
C 37	285.6	10.6	2299	10	AF3333331	Mus muscu
C 38	282.6	10.5	4308	5	AF205066	Gallus ga
C 39	243.6	9.0	1978	9	AF016709	Homo sapi
C 40	240.8	8.9	1762	6	BD007172	Human P2X
C 41	240.4	8.9	2062	9	BC039015	Homo sapi
C 42	239.2	8.9	1389	9	HSP2X4PC	Y07684 H.sapiens m
C 43	239.2	8.9	1750	6	AR270268	Sequence
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens purinergic receptor P2X-like 1, orphan receptor, mRNA
(CDNA clone IMAGE:5176046), partial cds.
ACCESSION
BC033488
VERSION
BC033488.1
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 2738)
Srausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,P.S., Wagner,L., Shennen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Xsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,D., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Snailus,D.E., Schenck,A., Schein,J.E., Jones,S.J. and Marra,M.A. 2002 full-length generation and initial analysis of more than 15,000 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 2738)
Strausberg,R.
Direct Submission
Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanaavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK plate: 51 Row: m Column: 3

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 4885534.

FEATURES

source

1..2738

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/mol_type="mRNA"

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/clone="IMAGE:5176046"

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/note="Vector: pCMV-SPORT6"

ORIGIN

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Query Match          96.0%; Score 2585.2; DB 9; Length 2738;
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DB 149 GTGGCTCTCTCGCCAAAAGGCTACAGAGCGGACCTGGAAACCCAGTTTCCAT 208

QY 157 CATCACCAAACTCAAGGGTTTCGGTCACTCAGATCAAGAGCTTGGAAACCGGCTGT 216
DB 209 CATCACCAAACTCAAGGGTTTCGGTCACTCAGATCAAGAGCTTGGAAACCGGCTGT 268

QY 217 GGATGTGCGCACTCTGTGAAGCCACCTCAGGAGAGAAAGCTGTCTTCTTGTGTACCAA 276
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QY 277 CTTCTTGTGACCGCCAGCCCAAGTTCAAGGAGATGCCCAGACACCCGTCCTCCACT 336
DB 329 CTTCTTGTGACCGCCAGCCCAAGTTCAAGGAGATGCCCAGACACCCGTCCTCCACT 388

QY 337 GGCTAACTGCTGGGTTCAGCAGGAGTGCCTCCGAAAGGGAGGGGACACACAGCCACCG 396
DB 389 GGCTAACTGCTGGGTTCAGCAGGAGTGCCTCCGAAAGGGAGGGGACACACAGCCACCG 448

QY 397 TGTAAAACAGCCAGCTGTGTGTGTTCATTTGAAGCCCAAGAGCTGTGAGATCTGGAG 456
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DB 509 TTGCTGCCAGTGGAGAGTGGCTGTGTGCTTCAGGCCCCCTGTGCCCCAGGCCCCAGAA 568

QY 517 CTTCACTGTTCATCAAAAACACAGTCACTTCAAGAGTTCACTTCTTAAGTCCAA 576
DB 569 CTTCACTGTTCATCAAAAACACAGTCACTTCAAGAGTTCACTTCTTAAGTCCAA 628

QY 577 TGCTTTCAGAGCTGGGACCCCACTATTTTAAAGCACTGCGCTATCAACCAATTCAG 636
DB 629 TGCTTTCAGAGCTGGGACCCCACTATTTTAAAGCACTGCGCTATCAACCAATTCAG 688

QY 637 CCCCTACTGTCCCGTGTTCGGCATTTGGGACCTCGTGGCCAAAGGCTGGAGGACCTTCGA 696

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DB 689 CCCCTACTGTCCCGTGTTCGGCATTTGGGACCTCGTGGCCAAAGGCTGGAGGACCTTCGA 748
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DB 749 GGACCTGGGCTGTCTGGGTGGCTCTAGGATCAGAGTTCACTGGGATGTGACTGGA 808
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QY 817 CTTTCAGAGAGCAGCTCACTGTGGGAGCAAGCGGGTGTGGAGGCCGCCCTCTCAA 876
DB 869 CTTTCAGAGAGCAGCTCACTGTGGGAGCAAGCGGGTGTGGAGGCCGCCCTCTCAA 928
QY 877 GCTCTATGAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGAGTTCGGGCTCAT 936
DB 929 GCTCTATGAATCCGCTTCGACATCTCTGTCACCGGGCAGGAGGAGTTCGGGCTCAT 988
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RESULT 3

AB002058

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

AB002058 3552 bp mRNA linear PRI 29-AUG-1997
 Homo sapiens mRNA for HUMAN P2XM, complete cds.

AB002058
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HUMAN P2XM.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)

Urano, T., Nishimori, H., Han, H., Furuhashi, T., Kimura, Y., Nakamura, Y.

Cloning of P2XM, a novel human P2X receptor gene regulated by p53

Cancer Res. 57 (15), 3281-3287 (1997)

9242461

2 (bases 1 to 3552)

Nakamura, Y.

Direct Submission

Submitted (22-MAR-1997) Yusuke Nakamura, The Inst. of Medical

Science, The University of Tokyo, Lab. of Molecular Medicine, Human

Genome Center; 4-6-1, Shirokanedai Minato-ku, Tokyo, Minato-ku,
Tokyo 108, Japan (E-mail:yusuke@ims.u-tokyo.ac.jp,
Tel:81-3-5449-5372, Fax:81-3-5449-5433)
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ORIGIN

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ORGANISM	BC064805	2578 bp	mRNA	linear	PRI 13-JAN-2004
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AUTHORS	BC064805	2578 bp	mRNA	linear	PRI 13-JAN-2004

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staudt, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toehiyuki, S., Carrincci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, E.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932	2 (bases 1 to 2578)	
Strausberg, R.		
Direct Submission		
Submitted (02-JAN-2004)	National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
NIH-MGC Project URL:	http://mgc.nci.nih.gov	
Contact:	MGC help desk	
Email:	cgapbs-remail.nih.gov	
Tissue Procurement:	Life Technologies, Inc.	
cDNA Library Preparation:	The I.M.A.G.E. Consortium (LLNL)	
cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by:	Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada	
info@bcgsc.bc.ca		
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzywinski, Reta Kutische, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.		
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Series:	IRAK Plate: 119 Row: d Column: 3	
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885534		
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ORIGIN

Query Match 88.5%; Score 2382.8; DB 9; Length 2578;

Best Local Similarity 94.4%; Pred. No. 0;

Matches 2542; Conservative 0; Mismatches 2; Indels 148; Gaps 1;

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QY	62	ACAGGCTGGGGCTTCTGGATTATAAGACGAGAGTGGGCTCTCTCGCCCAAAAAGGC	121
DB	74	ACAGGCTGGGGCTTCTGGATTATAAGACGAGAGTGGGCTCTCTCGCCCAAAAAGGC	133
QY	122	TACAGGAGCGGAGCTCGAACCCCGATTTTCCATCATCAACAACTCAAAAGGGTTTC	181
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QY	182	GTCACCTCAGATCAAGAGCTTGGAAACCGCTGTGGGATGTGGCGACTTCGTGAAGCCA	241
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QY	242	CTTCAGGGAGAGAACGTGTCTTCTTGTGGTACCACACTTCCTTGTGAACCCAGCCCAAGTT	301
DB	254	CCTCA-----	258
QY	302	CAGGSCAGATGCCAGAGACACCGTCCCTCCACTGGCTAACTGCTGGGTGCAGAGGAC	361
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QY	422	TTCAATGGGACCCACAGACCTGTGAGATCTGGAGTTGGTCCCGAGTGGAGTGGGTT	481
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QY	602	TATTTTACGACTGCGGTATGACCAAAATTCAGCCCTACTGTCCCGTTCGCGATT	661
DB	466	TATTTTACGACTGCGGTATGACCAAAATTCAGCCCTACTGTCCCGTTCGCGATT	525
QY	662	GGGACCTCGTGGCCAAAGCTGGAGGACCTTCAGAGACCTGGGCTTCTGGGTGGCTCT	721
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QY	722	GTAGGCATCAGATTTCATGGGATTTGACCTGGACACCGGGGACTCTGGGTCTGGCCT	781
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QY	1262	TTCCCTGCTGTTGAGATTGGGGCTGGAAAGGCGGGCCCTGCTGGGATCTCAAG	1321
DB	1126	TTCCCTGCTGTTGAGATTGGGGCTGGAAAGGCGGGCCCTGCTGGGATCTCAAG	1185
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QY	1742	GCAGAAAGGAGGTGATGGGGAGGGGATTTGTTTTCAGCTTCTCTGGTCTGTGATGCC	1801
DB	1606	GCAGAAAGGAGGTGATGGGGAGGGGATTTGTTTTCAGCTTCTCTGGTCTGTGATGCC	1665
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QY	1862	CCAGGCAAGGGCGGAGCATGTCTTTGGGCGCCACACCTGCTTATGTTATGAGGACCGGCT	1921
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DB	1786	GCCTTCCAGTGTAGCCCTTTTGCATAGGAGTCTGGGAGAGAGAGAGGGCGGACAG	1845

QY 1982 GCTAAGTTGGTGATCATTTGGGTTCTTCAGGACCTTCTATATCCCTCCTCGGTAAACCCCC 2041
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QY 2042 AGCCCAACCCCTTGGAATCTTTTCCCTCCAGGCTTCTCAGAGCCCTGGGGTGGAGGCTG 2101
Db 1906 AGCCCAACCCCTTGGAATCTTTTCCCTCCAGGCTTCTCAGAGCCCTGGGGTGGAGGCTG 1965
QY 2102 TGGGAGGCTGTACATCTGAATTCATTCAGTCAAGTCATACCTAGGAGCTGTCTGGG 2161
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QY 2522 AGTGGGAGACAGGCGCCCTGAGGCTGGGTATCCAGAGGGGCGACGTGCACTGATT 2581
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DEFINITION complete sequence.
AC002472
VERSION AC002472.8 GI:24137490
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 147086)
JOURNAL Budarf, M.L. and Emanuel, B.S.
REFERENCE 2 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Lao, V. and Roe, B.A.
JOURNAL Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCLR2-GGT Region
REFERENCE 3 (bases 1 to 147086)
AUTHORS Zhang, G., Lao, V., Zhan, M. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (20-AUG-1997) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
4 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (10-SEP-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
5 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (23-OCT-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
6 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (13-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
7 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (18-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
8 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (21-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
9 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (14-APR-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
10 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (13-SEP-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
11 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (13-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
12 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (19-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
13 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (20-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
14 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
15 (bases 1 to 147086)
AUTHORS Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
JOURNAL Direct Submission
TITLE Submitted (01-SEP-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 16 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (19-OCT-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	1713	GGCTGTGAGCTGGAGCCAAAGAGCAAGGAGGAGTGTATGATGGGAGGGGATT	1772
REFERENCE AUTHORS TITLE JOURNAL	OK 73019, USA 17 (bases 1 to 147086) Zhang, G., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A. Direct Submission Submitted (09-APR-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	171221	GGCTGTGAGCTGGAGCCAAAGAGCAAGGAGGAGTGTATGATGGGAGGGGATT	71280
COMMENT	On Oct 19, 2002 this sequence version replaced ei:22597497. Because these overlapping clones came from different libraries.	1773	GTTCAGCTTCTCTGGTGTCTGTGATGTCGCCAGGAGAGTCTTAATCTAGGGAATGGGGTGG	1832
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		171461	GTCTGGGAGAGAGAGGCGGCGGAGGCTAAGTGTGATCATATTGGGTCTCTCAGGA	71520
		2013	CCTTCTATATCCCTCTCGGTAAACCCCGACCCCAACCCCTTTGGAATCTTTCTCCAGGC	2072
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		2073	TTCTTGAGAGCCCTGGGGGTGGGAGGCTGTGGGAGGCTGTACATCTGAATTCATCTCAG	2132
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		2193	CCAGGCTGGATGGAGTGGCTGGGAAGGAATGGTTCCAAACACACCACCGAGATCTCCCTC	2252
		171701	CCAGGCTGGATGGAGTGGCTGGGAAGGAATGGTTCCAAACACACCACCGAGATCTCCCTC	71760
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		171761	AGGCTGGCCAGGTTTTCAGCTGGAAATCTCTCTTGTCTCCAGGGCGGCGCAGGGAATT	71820
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		171821	CTAAGTGTCCACCCAGGAGGCAAGGGGCTGTCTTCCACTGTGGTACCTGTGTGATCAG	71880
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		171881	GGCAAGCTGTGGAGGGCCAGGGGTGGGCTGAGACTGGGCTGACATCTAGAATCACCTGC	71940
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ACCESSION	AC007664			
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KEYWORDS	HTG.			

SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 162470)	
JOURNAL	Zhan,M. and Roe,B.A.	
REFERENCE	Homo sapiens 22q11 BAC Clone b453h4 In The BCRL2-GGT Region	
AUTHORS	Unpublished	
TITLE	2 (bases 1 to 162470)	
JOURNAL	Zhan,M. and Roe,B.A.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (15-SEP-1999) Department Of Chemistry And Biochemistry,	
TITLE	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
JOURNAL	OK 73019, USA	
REFERENCE	3 (bases 1 to 162470)	
AUTHORS	Zhan,M. and Roe,B.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-SEP-1999) Department Of Chemistry And Biochemistry,	
REFERENCE	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
AUTHORS	OK 73019, USA	
TITLE	4 (bases 1 to 162470)	
JOURNAL	Zhan,M. and Roe,B.A.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (18-SEP-1999) Department Of Chemistry And Biochemistry,	
TITLE	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
JOURNAL	OK 73019, USA	
REFERENCE	5 (bases 1 to 162470)	
AUTHORS	Zhan,M. and Roe,B.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry,	
REFERENCE	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
AUTHORS	OK 73019, USA	
TITLE	6 (bases 1 to 162470)	
JOURNAL	Zhan,M. and Roe,B.A.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (09-APR-2003) Department Of Chemistry And Biochemistry,	
TITLE	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
JOURNAL	OK 73019, USA	
COMMENT	On Sep 18, 1999 this sequence version replaced gi:5882763.	
FEATURES	Because these overlapping clones came from different libraries.	
Source	Location/Qualifiers	
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	/organism="Homo sapiens"	
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	/clone="b453h4"	
ORIGIN		
Query Match	59.1%; Score 1592.6; DB 9; Length 162470;	
Best Local Similarity	99.7%; Pred. No. 0;	
Matches 1595; Conservative	0; Mismatches 4; Indels 0; Gaps 0;	
QY	1053 ATGAGGAGCCCAAGGCCCGAAGCAACCGCAACTCTGTGTGGAGGAGCTGGCCCTTG 1112	
Db	26657 ATCTGAGCCCAAGGCCCGAAGCAACCGCAACTCTGTGTGGAGGAGCTGGCCCTTG 26716	
QY	1113 CATCCCAAGCCGACTGGCCGAGTGCTCAGACGAGCTCAGACCTGCACCCAGGCCA 1172	
Db	26717 CATCCCAAGCCGACTGGCCGAGTGCTCAGACGAGCTCAGACCTGCACCCAGGCCA 26776	
QY	1173 CTGCTCTGGAGTCAGACACAGACACCAAGGATGCCCTGTCCAAAGTTCTGACACCCACT 1232	
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QY	1293 AGGCGGGGCCCTGCTGGGGATCTCAAGGATGAGGCCCCAGCATGGAGGATTGGGGGTA 1352	
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QY	1413 CTGCTCAGGAGCCCATAGAGTGGCTGTGTTTGTAGACGCGGACAGAACTGACCCGT 1472	
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QY	1473 GGAGACTGGGAGAGCCCAAGCAGGCACTGTATTGACGGGCTCCGACTGCATGTGACAGG 1532	
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DEFINITION Homo sapiens DNA for Human P2XM, complete cds.
ACCESSION AB002059
VERSION AB002059.1 GI:2350848
KEYWORDS Human P2XM.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Urano,T., Nishimori,H., Han,H., Furuhashi,T., Kimura,Y., Nakamura,Y.
and Tokino,T.
TITLE Cloning of P2XM, a novel human P2X receptor gene regulated by p53
JOURNAL Cancer Res. 57 (15), 3281-3287 (1997)
MEDLINE 97384966
PUBMED 9242461
REFERENCE 2 (bases 1 to 28984)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1997) Yusuke Nakamura, The Inst. of Medical
Science, The University of Tokyo, Lab. of Molecular Medicine, Human
Genome Center; 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
(E-mail: yusuke@ims.u-tokyo.ac.jp, Tel:81-3-5449-5372,
Fax:81-3-5449-5433)

FEATURES
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RESULT 8
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DEFINITION Sequence 2 from patent US 6255472.
ACCESSION AR161588
VERSION AR161588.1 GI:16227535
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 1697)
AUTHORS Tokino,T. and Nakamura,Y.
TITLE Isolated nucleic acid molecule encoding a human skeletal muscle-specific receptor
JOURNAL Patent: US 6255472-A 2 03-JUL-2001;
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LOCUS Human mRNA for P2XM protein complete cds. 1697 bp DNA linear PAT 28-JUL-1999
DEFINITION
ACCESSION E17366
VERSION E17366.1 GI:5712049
KEYWORDS JP 199826281-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1697)
AUTHORS Tokino T. and Nakamura Y.
TITLE HUMAN GENE

JOURNAL
COMMENT
Patent: JP 199826281-A 2 06-OCT-1998;
OTSUKA PHARMACEUT CO LTD
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FN JP 199826281-A/2
PD 06-OCT-1998
PF 26-NAR-1997 JP 1997093044
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PC C12N15/09, A61K48/00, C07H21/04, C07K16/32, C12P21/02,
PC C12Q1/68,
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DEFINITION (cDNA clone C22ORF.pGEM.P2RXL1).
ACCESSION CR456535
VERSION CR456535.1 GI:47678600
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1517)
Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A.,
Cole, C.G., Goward, M.E., Aguado, B., Mallia, M., Mokrab, Y.,
Huckle, E.J., Beare, D.M. and Dunham, I.
Direct Submission
Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: c22@sanger.ac.uk Manuscript
Sanger Institute name: PGEM.P2RXL1
Homo sapiens cDNA sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to isolate cDNA clones
representing the full length open reading frame of well annotated
protein coding genes on human chromosome 22. For more information
see <http://www.sanger.ac.uk/HGP/Chr22/>.
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ORGANISM Unclassified.
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AUTHORS Tokino,T. and Nakamura,Y.
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 HUMAN GENE
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 VERSION AB010883.1 GI:2842547
 KEYWORDS mP2X; mP2X receptor.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

 REFERENCE
 AUTHORS Nawa,G., Miyoshi,Y. and Nakamura,Y.
 TITLE Cloning of mouse P2X receptor gene, regulated by p53, and identification of its genomic structure
 JOURNAL Published Only in DataBase (1998)
 REFERENCE 2 (bases 1 to 1484)
 AUTHORS Nawa,G., Miyoshi,Y. and Nakamura,Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-1998) Yusuke Nakamura, Osaka University Medical School, Division of Clinical Genetics, Biomedical Research Center, 2-2, Yamadaoka, Suita, Osaka 565, Japan
 E-mail:REGI-W@asahi-net.or.jp, Tel:81-6-879-3381, Fax:81-6-879-3389

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